

WEST Search History

DATE: Monday, March 03, 2003

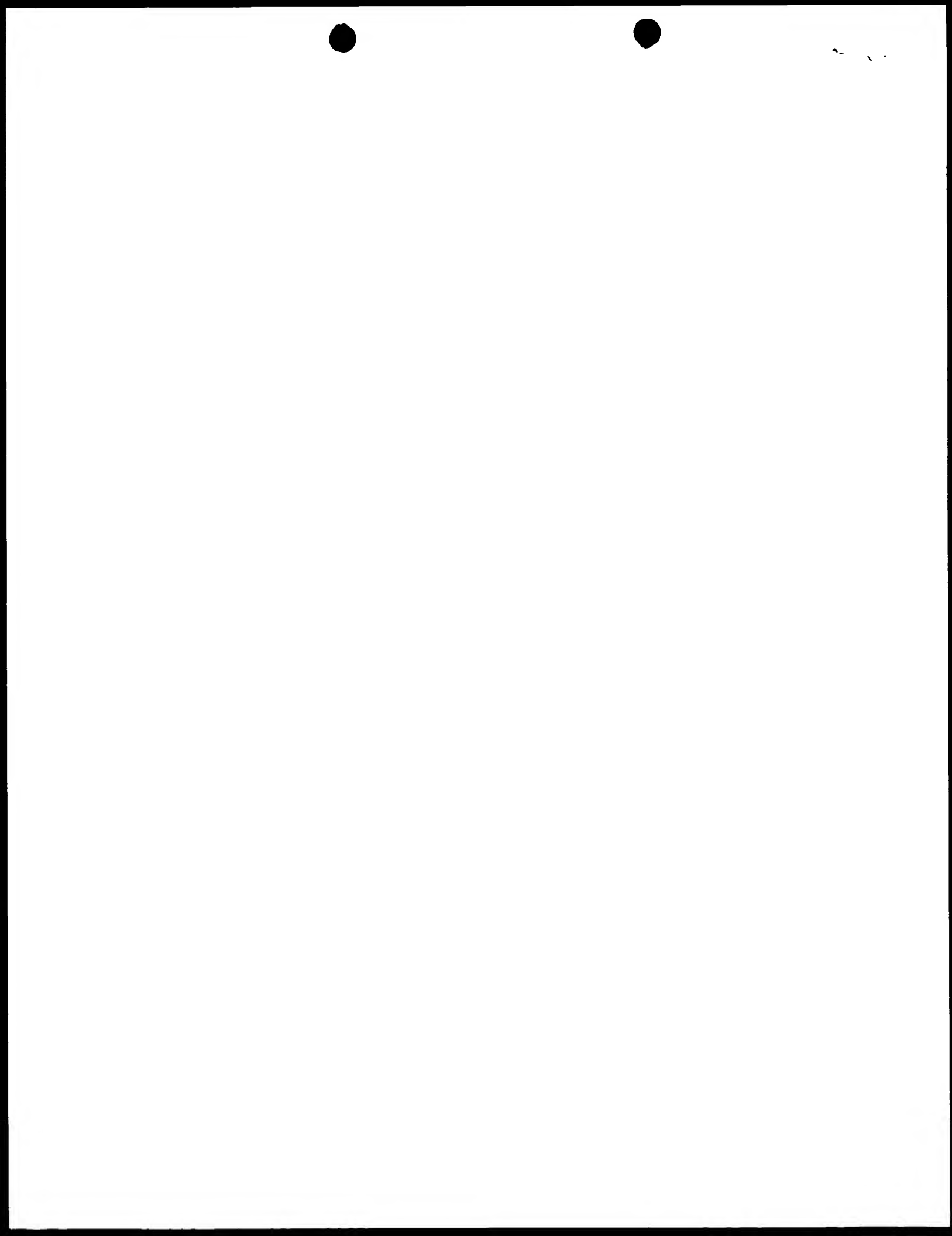
<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
L36	L33 and l14	1	L36
L35	L33 and l13	1	L35
L34	L33 and l12	0	L34
L33	L32 and l17	3	L33
L32	sodium-potassium adenosine triphosphorylase	3	L32
L31	L17 and l4	2	L31
<i>DB=USPT; PLUR=YES; OP=ADJ</i>			
L30	l17 and l4	1	L30
L29	compound or composition or agent	948383	L29
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L28	L4 and l20	1	L28
L27	L4 and l19	2	L27
L26	L4 and l18	0	L26
L25	L4 and l5	1	L25
L24	l5 same l4	0	L24
L23	l19 and l10	1	L23
L22	l20 and l10	1	L22
L21	l20 and l10	1	L21
L20	L13 with l9	46	L20
L19	L12 with l9	5	L19
L18	l14 with l9	38	L18
L17	l15 adj L16	824	L17
L16	transgenic	26173	L16
L15	rat or mouse or rodent	229213	L15
L14	L11 adj l3	13427	L14
L13	L11 adj l2	29140	L13
L12	L11 adj l1	27712	L12
L11	method	5683044	L11
L10	Dahl Salt sensitive rat	11	L10
L9	hypertension	35041	L9
L8	blood pressure or life span or renal pathology	52471	L8
L7	l4 with l5	0	L7
L6	L5 adj gene	2	L6



..

L5	hypertension susceptibility	10	L5
L4	Na,K-ATPase	83	L4
L3	screening	148614	L3
L2	identifying	267653	L2
L1	assaying or testing	463978	L1

END OF SEARCH HISTORY



10/040-722-9 01/4394:0
attached
STIC-Biotech/ChemLib

From: Whiteman, Brian
Sent: Monday, March 03, 2003 2:41 PM
To: STIC-Biotech/ChemLib
Subject: seq search

CRFC
10/040,722 filed 1/7/02 CON of 09/653,030 9/1/00
Ruiz-Opazo

search seq id no: 3 against public DNA databases.

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4992

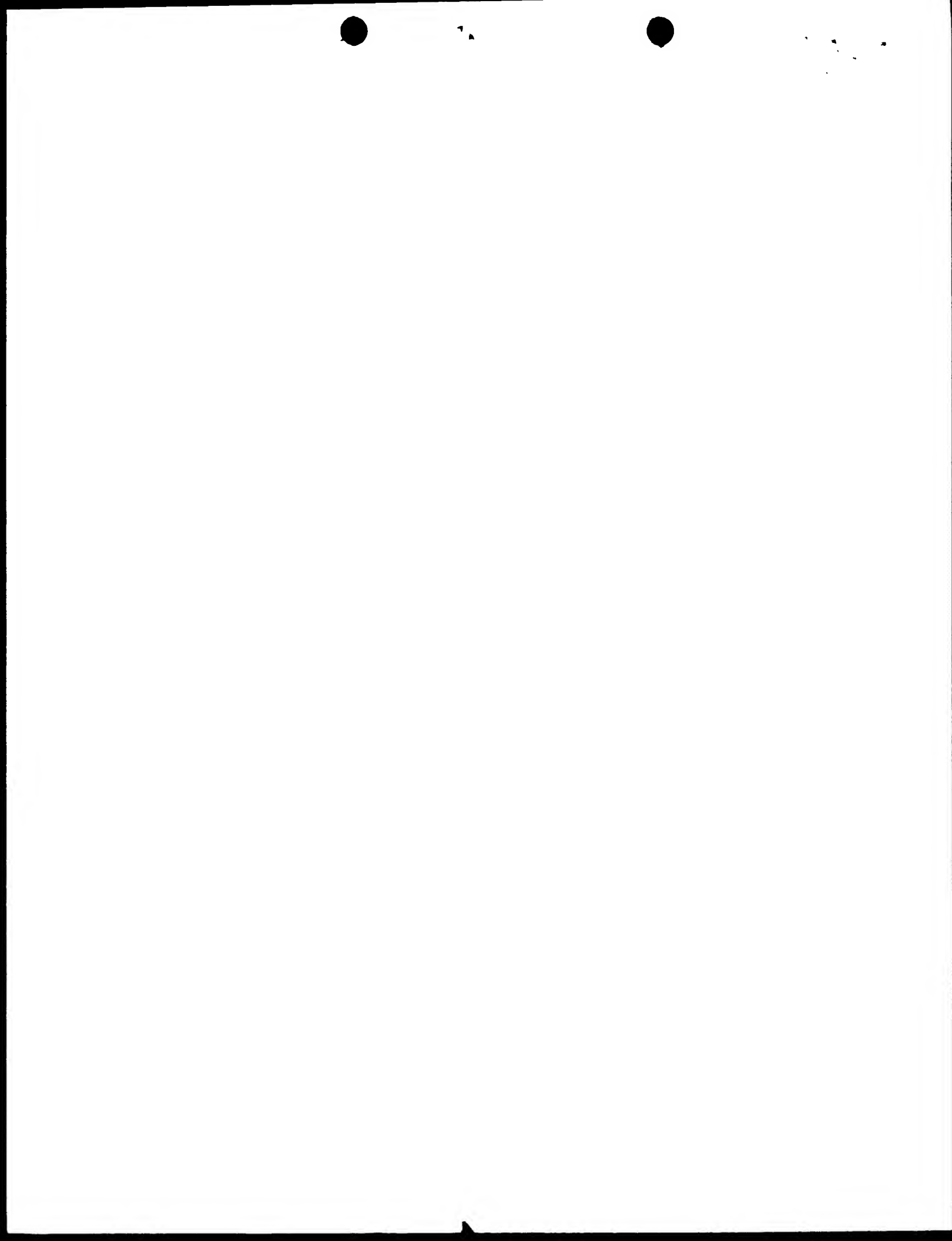
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Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



SEARCH REQUEST FORM

Requestor's

Name: _____

Serial

Number: _____

Date: _____

Phone: _____

Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 03-11-03

Searcher: ~~122~~ Beverage 404994

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

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Type of Search

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_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG Suite

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

Tue Mar 11 14:23:37 2003

us-10-040-722-3.rge

NH Termian
10/040-722 Page 1
Berg 10 3

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2003, 15:54:21 ; Search time 9230 Seconds
(without alignments)

11464.551 Million cell updates/sec

Title: US-10-040-722-3
Perfect score: 1 3636
Sequence: 1 3636

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 37: em_hlg_vrt:*
- 38: em_sy:*
- 39: em_hlg_hum:*
- 40: em_hlg_mus:*
- 41: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3631.2	99.9	3636	6	ARI75898	ARI75898 Sequence
2	3631.2	99.9	3636	10	RATATPA1	M14511 Rat Na+, K+-
3	3626.4	99.7	3636	6	ARI75895	ARI75895 Sequence
4	3626.4	99.7	3636	6	ARI75896	ARI75896 Sequence
5	3621.6	99.6	3636	6	ARI75897	ARI75897 Sequence
6	3347.6	92.1	3407	10	RATNKATP1	D10359 Rattus norv
7	3347.6	92.1	3407	10	RATNKATP1	X05882 Rat mPNA fo
8	3312.4	91.1	3648	10	BC021496	BC021496 Mus muscu
9	3312.4	91.1	3669	10	BC021496	BC021496 Mus muscu
10	3312.4	91.1	3686	10	BC021496	BC021496 Mus muscu
11	3310.8	91.1	3733	10	BC032187	BC032187 Mus muscu
12	3310.8	91.1	3670	10	BC025627	BC025627 Mus muscu
13	3297.4	90.7	3599	10	RATNALPH1	BC032187 Mus muscu
14	3014.6	82.9	3297	10	BC010319	BC010319 Mus muscu
15	2865.8	78.8	3680	9	BC003077	BC003077 Homo sapi
16	2836.2	78.0	4108	9	HSATPAR	BC003077 Homo sapi
17	2836.2	78.0	4108	9	HOMNKATPA	X04297 Human mRNa
18	2683	73.8	3667	4	OATPMR	DO0099 Homo sapien
19	2666	73.3	3429	4	SSATPAR	X02813 Sheep mRNa
20	2471.2	68.0	3117	4	PIGATPSEN	X03928 Pig mRNa fo
21	2438	67.1	3111	4	DOGNKAA	M8445 Pig Na+, K+
22	2301.6	63.3	3535	5	CHKATPAS	L42173 Canis fami
23	2102.6	57.8	3393	5	BNKAAI	BC025037 Mus muscu
24	2071.2	56.9	3379	5	XLU04238	J03230 Chicken (Na
25	2069.4	56.5	3392	5	XLU0108	U0108 Xenopus lae
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29	1949	53.6	3497	5	AY028630	AF286372 Danio rer
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33	1931	53.1	3559	10	RATATPA3	M14513 Rat Na+, K+
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ALIGNMENTS

RESULT 1	ARI75898	ARI75898	3636 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	ARI75898	Sequence 8 from patent US 6309874.				
DEFINITION	ARI75898					
ACCESSION	ARI75898					
VERSION	ARI75898.1	GI:17917197				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1	(bases 1 to 3636)				
AUTHORS	Belusa, R.					
TITLE	Selection marker					
JOURNAL	Patent: US 6309874-A 8 30-OCT-2001;					
FEATURES	Location/Qualifiers					


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RESULT 2

RATATP1 3636 bp mRNA linear p00 27-Apr-1993
LOCUS
DEFINITION

RATATP1 Rat Na⁺,K⁺-ATPase alpha isoform catalytic subunit mRNA, complete cds.

ACCESSION M14511.1 GI:203026

VERSION 1

KEYWORDS ATPase; integral membrane protein.

SOURCE Rat male brain (strain CD) cDNA to mRNA, clone B1-4

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;

Rattus.

1 (bases 1 to 3636)

Shull, G.E., Greed, J. and Lingrel, J.B.

Molecular cloning of three distinct forms of the Na⁺,K⁺-ATPase

alpha-subunit from rat brain

Biochemistry 25 (25), 8125-8132 (1986)

87128908

Drat entry and computer-readable sequence of [1] kindly provided

by G.E.Shull, 18-Feb-1987.

Location/Qualifiers

1..3636

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/db_xref="taxon:10116"

/note="(Na⁺ and K⁺) ATPase, alpha catalytic subunit

precursor"

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TGESEPORSPDPTNENPLETRNIAFSTNCEVETAGIIVYTDRIVMGATLALAG
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QY 1861 TACCTAGAGCTGGGGGCTTGTGAGAGCGTGTGTAGATTCTTGCACCTCTCTTCTGCT 1920
 Db 1861 TACCTAGAGCTGGGGGCTTGTGAGAGCGTGTGTAGATTCTTGCACCTCTCTTCTGCT 1920
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 RESULT 3
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 LOCUS ARI75895
 DEFINITION Sequence 5 from patent US 6309874.
 ACCESSION ARI75895
 VERSION ARI75895.1 GI:17917194
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3636)
 AUTHORS Belusa, R.
 TITLE Selection marker
 JOURNAL Patent: US 6309874-A 5 30-OCT-2001;
 FEATURES
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 Query Match 99.7%; Score 3626.4; DB 6; Length 3636;
 Best Local Similarity 99.8%; Pred. No. 0;
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Db	3301	TACTACTAGCCCACTGCCCTGTGCACGCCGTGGAAACATTGTGCCACAACAATGCAACTTCACCCC	3360
OY	3361	TACCCCCCTTTTGTAACCTTCAGTCTGTGAGCTCGSAACTTACTACCTGGTAGAAGAACA	3420
Db	3361	TACCCCCCTTTTGTAACCTTCAGTCTGTGAGCTCGSAACTTCACCTGGTAGAAGAACA	3420
OY	3421	CCAAAGCATGTGGGGATCCAGACGCTCTGSAATGAACATGTACCTGTAAATGGGGGGTGG	3480
Db	3421	CCAAAGCATGTGGGGATCCAGACGCTCTGSAATGAACATGTACCTGTAAATGGGGGGTGG	3480
OY	3481	GGGGAGGCGCTGCCGAAAAAACCGTGAAGGGGACGACACGCGGGAAGGTTATAATGTG	3540
Db	3481	GGGGAGGCGCTGCCGAAAAAACCGTGAAGGGGACGACACGCGGGAAGGTTATAATGTG	3540
OY	3541	CCTTTTGTGTTTTGTAAAAAAGAAAACTTGAAAAGACTGAAGATTACGTTTATATCT	3600
Db	3541	CCTTTTGTGTTTTGTAAAAAAGAAAACTTGAAAAGACTGAAGATTACGTTTATATCT	3600
OY	3601	GGATTTTTACAAATTAAGATGGCTATTATTAACGGA	3636
Db	3601	GGATTTTTACAAATTAAGATGGCTATTATTAACGGA	3636
RESULT 4			
LOCUS AR175896 3636 bp DNA linear PAT 17-DEC-2001			
DEFINITION Sequence 6 from patent US 6309874.			
ACCESSION AR175896			
VERSION AR175896.1 GI:17917195			
KEYWORDS			
SOURCE unknown.			
ORGANISM unknown.			
REFERENCE Unclassified.			
AUTHORS 1 (bases 1 to 3636)			
TITLE Belusa, R.			
JOURNAL Selection marker			
FEATURES Patent: US 6309874-A 6 30-OCT-2001;			
Location/Qualifiers			
source 1..3636			
BASE COUNT 850 a 967 c 995 g 824 t			
ORIGIN			
Query Match 99.7%; Score 3626.4; DB 6; Length 3636;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3630; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
OY	1	GGAAGCTCGCGGAGAGGAGCGGACACGCTGGCAAGCGCGCGGCGGACGCGACGACGAGCG	60
Db	1	GGAAGCTCGCGGAGAGGAGCGGACACGCTGGCAAGCGCGCGGCGGACGCGACGACGAGCG	60
OY	61	GGGCGACAGCGGCGGCTCGATCCGGGGGCGCGCGCTCTCCCTTTCTCCGCGG	120
Db	61	GGGCGACAGCGGCGGCTCGATCCGGGGGCGCGCGCTCTCCCTTTCTCCGCGG	120
OY	121	CAGCGCTAGTTCCGCGCTCTCGGCTCCCGCGCTCCACTTCCACGCGGAGCTGCTCT	180
Db	121	CAGCGCTAGTTCCGCGCTCTCGGCTCCCGCGCTCCACTTCCACGCGGAGCTGCTCT	180
OY	181	CTCCTCTTTCTAGTCTCCAGCACAGGACC CGGGGCGCGGAGCGCGCACGCTGCTCT	240
Db	181	CTCCTCTTTCTAGTCTCCAGCACAGGACC CGGGGCGCGGAGCGCGCACGCTGCTCT	240
OY	241	GGGAAGGGGGTTGACGAGCAAACTATGAGCTCGACACTGTATCAGAAACATGGGAGCAAG	300
Db	241	GGGAAGGGGGTTGACGAGCAAACTATGAGCTCGACACTGTATCAGAAACATGGGAGCAAG	300
OY	301	AAGACCAAGAAAGCGAAGAAAGGAAAGCACTGACGAACTCAAAGAGAAAGTGTATG	360
Db	301	AAGACCAAGAAAGCGAAGAAAGGAAAGCACTGACGAACTCAAAGAGAAAGTGTATG	360

Dh	2521	GTGAAAGAGGTGCTGTGATTTGTATTTGATAAATTGAAGAAATTCATTGCTTACACCCCTAAAC	2580
Oy	2581	AGTAACTTCCGGAAATCAACCCCTCTTGATATTTATTTATGCAACATTTCCATCTGCC	2640
Dh	2581	AGTAACTTCCGGAAATCAACCCCTCTTGATATTTATTTATGCAACATTTCCATCTGCC	2640
Oy	2641	CTGGGTCACCCGTGACCATCTCTCTGATTTGACTTGGGACATGACATGGTCCCGCATCTCT	2700
Dh	2641	TGTGGACACCGTACCATCTCTCTGATTTGACTTGGGACATGACATGGTCCCGCATCTCT	2700
Oy	2701	CTGGCTATAAGAACAGGCTGAAAGTGACATCATGAGAGGACGCCGAAATCCCAAAAG	2760
Dh	2701	CTGGCTATAAGAACAGGCTGAAAGTGACATCATGAGAGGACGCCGAAATCCCAAAAG	2760
Oy	2761	GACAAACTTGTGAAACGAGCGCTGATCAGCATGGCCATATGACAGATCGGTATGATCCAG	2820
Dh	2761	GACAAACTTGTGAAACGAGCGCTGATCAGCATGGCCATATGACAGATCGGTATGATCCAG	2820
Oy	2821	GCCCTGGAGAGCTTCTGACTTATTTGTGATTTCTGGCTGAGAACGGTTTCCGCCCTTT	2880
Dh	2821	GCCCTGGAGAGCTTCTGACTTATTTGTGATTTCTGGCTGAGAACGGTTTCCGCCCTTT	2880
Oy	2881	CACCTTGGGGCATCCGAGAGACCTGGGATGACCGCTGGATTAATGATGTGGAGACACG	2940
Dh	2881	CACCTTGGGGCATCCGAGAGACCTGGGATGACCGCTGGATTAATGATGTGGAGAGACG	2940
Oy	2941	TACGGGACAGATGACCTTACAGACAGAGAGATTTGTGAGTTTCACTGACACAGGCC	3000
Dh	2941	TACGGGACAGAGATGACCTTACAGACAGAGAGATTTGTGAGTTTCACTGACACAGGCC	3000
Oy	3001	TTCTTTGCTAGTATCTGTGTAGTGCAGTGGGCTGACTTGTGCATCTGTGAACACGAAAG	3060
Dh	3001	TTCTTTGCTAGTATCTGTGTAGTGCAGTGGGCTGACTTGTGCATCTGTGAACACGAAAG	3060
Oy	3061	AATTCGTCTTCCAGCAGGGAGATGAAAGAACAGATCTTAATTTTGGCCTCTTGAAGAG	3120
Dh	3061	AATTCGTCTTCCAGCAGGGAGATGAAAGAACAGATCTTAATTTTGGCCTCTTGAAGAG	3120
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Dh	3121	ACAGCTCTTGTGCTTTCTGTCTTCTACTGCCCTCTGGGATGGGTGGACCCCTTGAAGATGAT	3180
Oy	3181	CCCCCTCAACCTACTTGGTGTCTGTGACCTTCCCTACTCCCTCTCATCTTCTGTGAT	3240
Dh	3181	CCCCCTCAACCTACTTGGTGTCTGTGACCTTCCCTACTCCCTCTCATCTTCTGTGAT	3240
Oy	3241	GACGAGTGGGAGACTATCATCAGGAGAGACCCCTGGCGGCTGGGTGGAGAAAGAACCC	3300
Dh	3241	GACGAGTGGGAGACTATCATCAGGAGAGACCCCTGGCGGCTGGGTGGAGAAAGAACCC	3300
Oy	3301	TACTACTAGCCACTGACCTGTGACGCGCGTGAACATTGTGTCANACATGACCTTACCCC	3360
Dh	3301	TACTACTAGCCACTGACCTGTGACGCGCGTGAACATTGTGTCANACATGACCTTACCCC	3360
Oy	3361	TACCCCCCTTTGTGACTTCAAGCTTGTGAGCTCGGAACCTTACCTGTGAGAAAGCA	3420
Dh	3361	TACCCCCCTTTGTGACTTCAAGCTTGTGAGCTCGGAACCTTACCTGTGAGAAAGCA	3420
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Dh	3421	CCAAGCATGTGGGATTCAGACGCTCTGGAATGAAAGCATGTAGTGTAAATGGGGGGCGG	3480
Oy	3481	GGGAGGCGCTGCCGGAAGAAACACCGTGTGACGGGAGACAGACGCGGGAGAGTTTAATGTG	3540
Dh	3481	GGGAGGCGCTGCCGGAAGAAACACCGTGTGACGGGAGACAGACGCGGGAGAGTTTAATGTG	3540
Oy	3541	CCTTTGTGTTTGTAAAAAAGGAAAACTGGAAAGCATGAAGATTACGTTTATATCT	3600
Dh	3541	CCTTTGTGTTTGTAAAAAAGGAAAACTGGAAAGCATGAAGATTACGTTTATATCT	3600
Oy	3601	GGATTTTACAATTAAGATGCTATTATTAACGGA 3636	
Dh	3601	GGATTTTACAATTAAGATGCTATTATTAACGGA 3636	

RESULT 5	AR175897	3636 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR175897	Sequence 7 from patent US 6309874.			
DEFINITION	Sequence 7 from patent US 6309874.				
ACCESSION	AR175897				
VERSION	AR175897.1	GI:17917196			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 3636)				
AUTHORS	Belusa,R.				
TITLE	Selection marker				
JOURNAL	Patent: US 6309874-A 7 30-OCT-2001;				
FEATURES	Location/Qualifiers				
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	/organism="unknown"				
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ORIGIN					
Query Match	99.6%; Score 3621.6; DB 6; Length 3636;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 3627; Conservative	0; Mismatches 9; Indels 0; Gaps 0				
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QY	61	GGCGGACGACGCGCGGCGGCTCGGATCCGGGCGCGCGCGCGCTCTCCCTCTTCTCGGGCG 120			
Db	61	GGCGGACGACGCGCGGCGGCTCGGATCCGGGCGCGCGCGCGCTCTCCCTCTTCTCGGGCG 120			
QY	121	CAGCCCTAGTTCCTCGGCTCTCGGCTCCCGGCTCCCACTCTCCAGCGGAGCTGCTT 180			
Db	121	CAGCCCTAGTTCCTCGGCTCTCGGCTCCCGGCTCCCACTCTCCAGCGGAGCTGCTT 180			
QY	181	CTCCTCTTTCTAGTCTCCAGCCACAGACCGCGCGCGGCGCGCGCGCGGCGGACATG 240			
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QY	241	GCGAAGGGGCTGGACGAGCAAGATGAGCCCGGAGCTGTATGAAATGCGGACAG 300			
Db	241	GCGAAGGGGCTGGACGAGCAAGATGAGCCCGGAGCTGTATGAAATGCGGACAG 300			
QY	301	AGAGCAGAAAGGCGAAGAGAAAGGACATGGACGAACTCAGAGAGAGAGTGTATG 360			
Db	301	AGAGCAGAAAGGCGAAGAGAAAGGACATGGACGAACTCAGAGAGAGAGTGTATG 360			
QY	361	GACGACCAATAAATCAGCTGATGAACTGCATCGTAAATACGAAACGATTTGAGCGGA 420			
Db	361	GACGACCAATAAATCAGCTGATGAACTGCATCGTAAATACGAAACGATTTGAGCGGA 420			
QY	421	GCGCTTAACACCCGCAAGGCGCGTGAATCTGAGCTCGGAGTAGGCCCAACGCCCTCACG 480			
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QY	481	CGCCCTCCCACTACTCCGAGTGCTCAATTTCTGTGCGAGCTGTTCGAGCTTCTCC 540			
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Db	541	ATGTACTGTGATTTGGAGCCATTTTGTGTTCTTGTGCTTATGGCATCGAAGTGTACA 600			
QY	601	GAAAGGAAACCAACCAATGATCTGTAACCTCGGGGCTCGTGTGCTGTGCTGATC 660			
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QY	661	ATAACTGGCTTTCTCTATTAACAAGCAAAAGCTCAAGATCATGGAATCTTTC 720			
Db	661	ATAACTGGCTTTCTCTATTAACAAGCAAAAGCTCAAGATCATGGAATCTTTC 720			

COMMENT
Found by the N-terminal amino acid sequence of the mature alpha-subunit
additional amino acid residues were cleaved during the
post-translational processing, and pRNL1 was found to carry a
cDNA encoding the alpha subunit of the rat kidney type.
Location/Qualifiers
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30. .3083
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CDS

sig_peptide
mac_peptide

BASE COUNT 822 a 881 c 913 g 791 t

ORIGIN

Query Match 92.1% Score 3347.6; DB 10; Length 3407;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3383; Conservative 0; Mismatches 19; Indels 4; Gaps 2;

QY	228	CGCCGCCACCATGGGGAAGGGGCTTGACGACAGCATGTAGCCCGCAGCGTGTATCAGA	287
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OY	288	ACATGGGGACAAAGAACCAAGAAAGGCGAAAGAAAGGACATGACGAACTTAAGAA	347
Db	65	ACATGGGGACAAAGAACCAAGAAAGGCGAAAGAAAGGACATGACGAACTTAAGAA	124
OY	348	GGAAGTGTCTATGACGACACATAAATCAGCTGGATATACCTCATCTCTAAATACGAAC	407
Db	125	GGAAGTGTCTATGACGACACATAAATCAGCTGGATATACCTCATCTCTAAATACGAAC	184
OY	408	AGATTTAGCCGAGGCTTAACAACCCGCAAGGCGCGCTGAGATCTTGCTCGGGATGCCCC	467
Db	185	AGATTTAGCCGAGGCTTAACAACCCGCAAGGCGCGCTGAGATCTTGCTCGGGATGCCCC	244
OY	468	CAAGCCCGCTCAAGCCCGCTCCACACTACCCGAGTGGGCTCAAAATTCGTGGGAGCTTT	527
Db	245	CAAGCCCGCTCAAGCCCGCTCCACACTACCCGAGTGGGCTCAAAATTCGTGGGAGCTTT	304
OY	528	CGGTGGCTTTCATGTTACTGTGATGTGAAGCCATTCCTTGTGTTCTTGAGCTATAGCAT	587
Db	305	CGGTGGCTTTCATGTTACTGTGATGTGAAGCCATTCCTTGTGTTCTTGAGCTATAGCAT	364
OY	588	CGGAAGTGTCTACAGAAAGAGAAACACCCAAATGATGATTTTAACTTCGGGGTCTGCTG	647
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RESULT 9
2001.100

DEFINITION Mus musculus, ATPase, Na+K+ transporting, alpha 1 polypeptide, J02486, MGC:38418, IMAGE:5346159. tRNA, complete cds.

VERSION BC021496.1 GI:18204492

ORGANISM Mus musculus
Phylum Chordata: Vertebrata: Euteleostomi:

REFERENCE 1 (bases 1 to 3669)

Submitted (14-JAN-2002) National Institutes of Health, Mammalian
[National Cancer] Reviewing Office

USA

Email: cgapbs-r@mail.nih.gov

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Gaithersburg, Maryland;

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Clone distribution: MGC clone distribution information can be found

This clone was selected for full length sequencing because it

FEATURES
analysts.
Location/Qualifiers

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/Classification: UNCLASSIFIED//FOR OFFICIAL USE ONLY

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Db	1495	TCAGACACCTGGTGGCTGTGCAAGAAATGGCTGGCTCTGTATAACAGGCGAGTGTTCAG	1554
QY	1540	GCTAACCAAGAAAACTGGCTTATCCTTAAGCTGACGTAAGCGGGAGAGTGGTTCGAGTGC	1599
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QY	1600	GGGCTCTTAAGTGAATGCAATGAGAGCTGCTGTGAGTCCGTAATGAGATGAGCGAGAAATAC	1659
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QY	1660	ACCAAGATAGTGAAGATTCCTCTTCAACTCCACCAACAGTACCAGCTTCATTCACAAG	1719
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Db	1795	CTGGAACCGCTGAGCTCCATCCTCTCTCAACGGAAGAGCAGCAGCTGATGAAGAGCTG	1854
QY	1840	AAGAGCGCTTTGAGAAATGCTTAACCTTAAGACTGTGGAGCGCTGTGTAGGT	1899
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QY	1900	TTCTGGCACTCTCTGTGACTGACGAACAGTTTCCGAAAGCTTCCAGTTTGAACATGAT	1959
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QY	1960	GAACTCAATTTCCCGGTGATAACTCTGCTTGGTGGGTCTTATCTCATGATTGACCT	2019
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[illegible]

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Db 777 AAGAAATATGATCTTCAAGAAAGCTTGTGATTTGAAATGAGAGAAATGAGATTAAC 836
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Db 837 GCGAGAGATGATCTTCAAGAAAGCTTGTGATTTGAAATGAGAGAAATGAGATTAAC 896
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Query Match 82.9% Score 3014.6; DB 10; Length 3297;
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aa Disclosure: Page 59-63; 72pp; English
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OY 2761 GACAAACCTTGTGAAGAGGCTTGTATGATGATGAGCTTATGAGACATGCTATGATCCG 2820
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OY 2821 GCGCTGGAGAGCTTCTTCACTTATTTGTGATTTGTGCTGAGAAAGGTTTCTGCGCTTT 2880
Db 2821 GCGCTGGAGAGCTTCTTCACTTATTTGTGATTTGTGCTGAGAAAGGTTTCTGCGCTTT 2880
OY 2881 CACCTGTTGGGACATCGAGAGACCTGGAGATGACCGCTGATCAATGATGTGAGAGACAGC 2940
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OY 2941 TACGGGACAGTGAACCTTACAGACAGAGAAAGATTGGAGATTACCTGACACAGGCC 3000
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Db 3121 ACAGCTGTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
OY 3181 CCCCTCAACCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
Db 3181 CCCCTCAACCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
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OY 3301 TACTACTAGCCCATGCTGCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3360
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Db 3541 CTTTTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600
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Db 3601 GGATTTTACAAATTAAGATGCTATTATTAACG3AA 3636

RESULT 2
AAS16480
ID AAS16480 standard; cDNA: 3636 BP.
XX
AC AAS16480;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat cDNA encoding partial wild-type (Na,K)-ATPase.
XX
KW Rat; ss; (Na,K)-ATPase; 799/801NKA; mutant; ouabain; gene therapy.
XX
OS Rattus rattus.
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FT /*partial.
FT /*note= "No start or stop codon"
FT 1..240
FT /*tag= b
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y	2701	CTGGCCCTATGAACAGGCTGGAAAGTGACATCATGGAAGGCAGCCAGAAATCCCAAAACG	2760
b	2701	CTGGCCCTATGMAACAGGCTGGAAAGTGACATCATGGAAGGCGCCCAAAAATCCCAAAACG	2760
y	2761	GACMAACTTGTAGACGAGCGCTGTATTCAGCATGGCCATATGGAACAGATCGGATGATCCAG	2820
b	2761	GACMAACTTGTGMAACGAGGCTGTATTCAGCATGGCCATATGGAACAGATCGGATGATCCAG	2820
y	2821	GGCCCTGGAGGCGCTCTTCACTATTATTGTGATTTCTGGCTGGAACCGGTTTCTGCCCTTT	2880
b	2821	GGCCCTGGAGGCGCTCTTCACTATTATTGTGATTTCTGGCTGGAACCGGTTTCTGCCCTTT	2880
y	2881	CACCTGTTGGGCAATCCGAAGACCTGGGATGACCCCTGGATTATATGATGAGAGACAGC	2940
b	2881	CACCTGTTGGGCAATCCGAAGAGCTGGGATGACCCCTGGATTATATGATGAGAGACAGC	2940
y	2941	TAGGGGAGAGAGTGACCTACAGAGCAGAGGAAGATTGGAGTTCACTGCCACAGGCCC	3000
b	2941	TAGGGGAGAGAGTGAGACTACAGAGCAGAGGAAGATTGGAGTTCACTGCCACAGGCCC	3000
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b	3001	TTCTTTTCAGTATCGGTTAGTAGAGAGTGGGCTGACTTGGTATCTGGCAAGCCAGAAAG	3060
y	3061	AATTCTGCTTCCAGCAGGGGAATGGAAGAACAAAGATCTTAAATATTTGGCCTCTTTGAAG	3120
b	3061	AATTCTGCTTCCAGCAGGGGAATGMAAGAAATMAATCTTAAATATTTGGCCTCTTTGAAG	3120
y	3121	ACAGCTTTGCTGCTTCTCTGTCTACTGCGCCCTGGGATGGGTGCAGCCCTTAGAGATGAT	3180
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b	3181	CCCCCTCAAACTACTGGTGGTTGTGACCTTCCGCCCTACCTCCCTTCTCATCTTCTGTAT	3240
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b	3241	GACGAGGTGGCGGAAGCTCATATCAGGCGAGCCCTGGCGGCTGGGTGAGAAAGMAAAC	3300
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b	3301	TACTACTAGCCCATCTGCCCTGCAGCGCGTGGGAAATTTGTGTGCATACATGCACTACCCC	3360
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b	3481	GGGAGAGGCGTCCCGAAAAACACCGTGGACGGGAGCGACACCGGGGAAAGGTTTATATGTG	3540
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b	3541	CGTTTGTGTTTTGTGTAAGAAAAAGAAAACTGTGAAGACGTGAAGAGTTACGTTTATATCT	3600
y	3601	GGATTTTACAAATAAAGATGGCTATTTATATAGGAA	3636
b	3601	GGATTTTACAAATAAAGATGGCTATTTATATAGGAA	3636
RESULT 3			
AAV84294			
ID	AAV84294 standard; DNA; 3636 BP.		
AC	AAV84294;		

RESULT 3
AAV84294
ID AAV84294 standard; DNA; 3636 BP.
XX
AC AAV84294;

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Qy 1261 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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Qy 1441 ACCAGAGAAATCAGAGTGTGATGATGATGATGATGATGATGATGATGATG 1500
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Qy 1501 TCCGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
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DB 421 GGCTTAACCCGCAAGGCGCGCTGAGATCTGGCTGGGATGGGCCCAAGCCCTCAAG 480
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DB 481 CCCCCCTCCACTACCCGAGTGGGTCAAAATCTGTGGGAGCTGTTGAGTGGCTTCC 540
QY 541 ATGTACTGTGATTTGAGAGCCATCTTTGTTCTTGAGCTTAATGGCATCGAATGTCA 600
DB 541 ATGTACTGTGATTTGAGAGCCATCTTTGTTCTTGAGCTTAATGGCATCGAATGTCA 600
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DB 601 GAAGAGAACCAACCAATGATGATCTGACTCGGGGTGGTGGTGGTGGTGGTGGTGGT 660
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DB 841 GATCTCAGAAATCATATCTGCAAAATGCTGCAAGGTGATTAATCTCTCACTGATGTA 900
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DB 1441 ACCACAGAGAAATCAGAGTGGGTCTCTTTGACAAAGACGTGACGACCTGATGCTG 1500
QY 1501 TCAGAAATTCGTGCTCTGTAAACAGGAGAGTGTTCAGGCTAAACAAAGAAAGCTGCT 1560

DB 1501 TCAGAAATTCGTGCTCTGTAAACAGGAGAGTGTTCAGGCTAAACAAAGAAAGCTGCT 1560
QY 1561 ATCTTAAGCGTGAAGTACCGGAGATGCTTCCGAGTGGGCTCTTAAAGTCAATGAG 1620
DB 1561 ATCTTAAGCGTGAAGTACCGGAGATGCTTCCGAGTGGGCTCTTAAAGTCAATGAG 1620
QY 1621 GTCTGCTGGCTCCGTGATGAGATGAGAGAGAGTACACCAAGATAGTGAAGATTCCT 1680
DB 1621 GTCTGCTGGCTCCGTGATGAGATGAGAGAGAGTACACCAAGATAGTGAAGATTCCT 1680
QY 1681 TTCAACTCCACCAACAACTACAGCTCTCAATTCACAAAGACCAAGCATCGAGCTT 1740
DB 1681 TTCAACTCCACCAACAACTACAGCTCTCAATTCACAAAGACCAAGCATCGAGCTT 1740
QY 1741 AAGCACTCTGATGATGATGAGAGGCCCCCAAGAAAGATCTGAGACGATGATGATC 1800
DB 1741 AAGCACTCTGATGATGATGAGAGGCCCCCAAGAAAGATCTGAGACGATGATGATC 1800
QY 1801 CTCTCCACGCGAAGAGACAGCCCTGAGACGAAAGCTGAAAGAGCCCTTGAGAAATGCC 1860
DB 1801 CTCTCCACGCGAAGAGACAGCCCTGAGACGAAAGCTGAAAGAGCCCTTGAGAAATGCC 1860
QY 1861 TACCTAAGCTGGGGGCTTGGAGAGGCTGCTAAGTTCTGACCACTCCTCTGCT 1920
DB 1861 TACCTAAGCTGGGGGCTTGGAGAGGCTGCTAAGTTCTGACCACTCCTCTGCT 1920
QY 1921 GACGAACAGTTTCCGAAAGCTTCCAGTTTGACATGATGAAGTCAATTTCCGATGAT 1980
DB 1921 GACGAACAGTTTCCGAAAGCTTCCAGTTTGACATGATGAAGTCAATTTCCGATGAT 1980
QY 1981 AACCTGTGCTGTCGAGCTTATCTTCATGATTAACCTCTCTGAGCTCTGTCCCGAT 2040
DB 1981 AACCTGTGCTGTCGAGCTTATCTTCATGATTAACCTCTCTGAGCTCTGTCCCGAT 2040
QY 2041 GCTGTGGGAAATGCGCGAGCGCTGGGATTAAGTCATGATGATGATGATGATGATGAT 2100
DB 2041 GCTGTGGGAAATGCGCGAGCGCTGGGATTAAGTCATGATGATGATGATGATGATGAT 2100
QY 2101 ATCAGACCCAAAGCCATTGCTAAAGGGGATGGGATTAATCTCAGAAAGTAAAGAGCTG 2160
DB 2101 ATCAGACCCAAAGCCATTGCTAAAGGGGATGGGATTAATCTCAGAAAGTAAAGAGCTG 2160
QY 2161 GAAGACATTCGTCGCCCTCAACATTCAGATGACACAGTGAACCCGAGATGGCAAG 2220
DB 2161 GAAGACATTCGTCGCCCTCAACATTCAGATGACACAGTGAACCCGAGATGGCAAG 2220
QY 2221 GCTGTGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
DB 2221 GCTGTGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
QY 2281 TTCCGCTACCAACCGAGATTTGTCTTTGCTAGAGCTTCTCCTCAAGAGCTCATCAT 2340
DB 2281 TTCCGCTACCAACCGAGATTTGTCTTTGCTAGAGCTTCTCCTCAAGAGCTCATCAT 2340
QY 2341 GTGAGAGGCTGCGAGGAGGAGAGGATGATGATGATGATGATGATGATGATGATGAT 2400
DB 2341 GTGAGAGGCTGCGAGGAGGAGAGGATGATGATGATGATGATGATGATGATGATGAT 2400
QY 2401 TCTCCAGCTTTGAAAAAGGAGATTTGGGGTTGCCATGGGGAATTTGGCTCGAGTGT 2460
DB 2401 TCTCCAGCTTTGAAAAAGGAGATTTGGGGTTGCCATGGGGAATTTGGCTCGAGTGT 2460
QY 2461 TCCAGAGAGCTGTGATGATTTCTTCTGATGATGATGATGATGATGATGATGATGAT 2520
DB 2461 TCCAGAGAGCTGTGATGATTTCTTCTGATGATGATGATGATGATGATGATGATGAT 2520
QY 2521 GTAGAGAGAGTGTCTGATTAATTAATCTTGAAGAAATCAATTTGATCAACCTTAACA 2580
DB 2521 GTAGAGAGAGTGTCTGATTAATTAATCTTGAAGAAATCAATTTGATCAACCTTAACA 2580
QY 2581 AGTAAATTCGGAATCACCCCTTCTGATTAATTAATTTGATGAAACATTTCCATGCTCC 2640

[illegible][illegible]

	CC	AAT57161 to AAT57576 represent cell and tissue specific polynucleotide sequences (1). (I) can have cytoskeletal, immunological and neuroprotective activities, and can be used in gene therapy. (1) and proteins (II) encoded by them are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.
	CC	
	CC	
	XX	
SO	Sequence 8914 BP, 2219 A, 2249 C; 2242 G; 2204 T; 0 other;	
	Query Match 70.4%; Score 2559.4; DB 22; Length 8914;	
	Best Local Similarity 87.2%; Pct. No. 0;	
	Matches 2896; Conservative 0; Mismatches 396; Indels 29; Gaps	
OY	21 CGACACGCTGGCGAGGTGGCGGCAGCGACGACGCGCAGCAGCGCGCGCTTC	80
Db	4394 CGACACGCTGGCGACACGCGGTACGAGCCCGCGCGCGCGACGACAGCGCGCGCATC	4453
OY	81 GGTCCGGGGCGCGCGCGCGTCCCTTTTC--TCCGGCGCACGCCAGTATCCGGCT	138
Db	4454 GCCCGAGCGCGCGCGCGCTTGCCACCTCCCGCCCGCGGACGCTTAGCTCCCTCA	4513
OY	139 CTCGGCTCCCCCGCGCTCCACTTCCCAGCTGGGAAGTGTCTCTCCCTC---TTCGTGT	194
Db	4514 CTGACTCCCTCGTACCCTGCTGCTGTGGCCGAGAGTGTCTGTCTTCTCTGATT	4573
OY	195 CTCGAGCCACAGAACCCGGCGCGCGGCGCGCGACGCGCTCACCATTGGGAAGGGGTTGG	254
Db	4574 CTCGAGCGACAGAACCCGGCGCGCGCGCATCTGAGCACCGCACATTGGGAAAGGGGTTGG	4633
OY	255 ACGAACAAGTATGAGCCCGCGAGCTGTATCAACAATGGGAGCAAGAAGAGCAACAAGGC	314
Db	4634 ACGTGTATGATGAGCTTGCAGCTGTTTCAACAAGAGTGTATAAAAAGCGAAGAAAGG	4693
OY	315 GAAGAAGAAAGGACATGAGCAAACTCAAGAAGAGTGTCTATGAGACGACCATTAAC	374
Db	4694 CAAAAAAGACAGGAGCATGATGAATCTGAAGAAAGAGTTCTATGATGATCATTAAC	4753
OY	375 CAGCTCGAGTAACTCCATCGTAAATATACGAAACAGATTGAGCGGAGCGCTAACACCGCC	434
Db	4754 TAGCTTGTATGAATCTTCACTGTAATATGAACAGACTTGAAGCCGGGAGTTAACATCTGC	4813
OY	435 AAGGCGCGGTGAGATCTTGGCTTCGGAGTGGCCCAAAGCCCTCAGCGCCCTCCCACTAC	494
Db	4814 TCGTGAGCTGAGATCTTGGCCCGCGAGATGATCCAAAGCCCTCAGCTCCCTCCACATAC	4873
OY	495 TCCCGAGTGGTCAATTCCTGTCGAGAGTGTTCGGTGGCTTCTCATATTAATCTGTGGAT	554
Db	4874 TCTTGATGATCAACTTTTGTGCGGAGCTCTTTGGGGGTTCTCAATGTACTGTGGAT	4933
OY	555 TGAGGCAATTTCTTTGTTCTTGGCTTATGGCATCCGAATGTGTACGAAGAGAAACAC	614
Db	4934 TGGAGGATTTCTTTGTTCTTGGCTTATGACATCCAAGCTGTACGAAGAGAAACCTCA	4993
OY	615 AAATGATGATCTGTACTCGGGGTGCTGTCTGTCTGTCTCATATATAATCTGGCTTT	674
Db	4994 AAACGTAATCTGTACTCGGGGTGTGTGTATCAAGCGTGTATATATATATCTGTGTTCT	5053
OY	675 CTCCTTATTCAAAGAAAGAAAGCTCCAAAGATCATGAATCTTCAAMAACATGGTCCC	734
Db	5054 CTCCTTACTTCAAGAAAGCTTAAAGATCATGAATCTTCAAAAACATGGTCCC	5113
OY	735 TCAGCAAGGCTTCGTGATTCGAAATGGAAGAGATGAGCATTAACGCAAGGATGTGGT	794

Db	5114	TCAGCAAGCCCTTGATTCGAAATGGTAGAAATGAGCATTAATGGCGAGGAAGTTGT	5173
Oy	795	CGTTGGTATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGCTGATCTCAAAATCAT	854
Db	5174	GGTTGGGGAGATCTGGTGGAAAGTAAAGAGAGAACCGAAATCTCTGGTGCCTCAAGAAATCAT	5233
Oy	855	ATCTGCAAAATGGCTGCGAAAGTGATTAATCCTCTCACTCACTGGTGATCAGAACCCGAC	914
Db	5234	ATCTGCAAAATGGCTGCGAAGGTGATTAATCCTCTCTCTCACTGGTGATCAGAACCCGAC	5293
Oy	915	TCGGTCCCGGAGATTTTCAAAAGAGAACCCCTTGGAGACAAAGAAACATTTGCTCTTCTC	974
Db	5294	TAGGTCTCCAGATTTTCAAAATGAAAAACCCCTCGAGACAGAGAAACATTTGCTCTTCTTC	5353
Oy	975	AACCAATGATGTTGAAGAGAACTGACAGTGGCATCTGTGTACATCGGGAGATCGAACGT	1034
Db	5354	AACCAATGATGTTGAAGAGACGCGAGGTGGTATTGTTGTCTACATCGGGAGATCGCACGT	5413
Oy	1035	GATGGGAGAGATCGCACCCCTTGCTCTTGAGGTGGAAGGCGGCTGACCCCATTTGCTGA	1094
Db	5414	GATGGGAAGAAATTTGCCACACTTCTCTTGAGGTGGAAGAGGCGCCACCATTTGCTGC	5473
Oy	1095	AGAAATGAGACATTCATCCACTCATACAGGGTGGCGCGGTCCCTGGGGAGTGTCTTT	1154
Db	5474	AGAAATGGAACATTTTATCCACATCATACAGGGTGGCTGTGTCTCGGGGTGTCTTT	5533
Oy	1155	CTTCATTTCTCTCTGTGATCTTTGAG-TACACCTGGCTCGAGGCTGTCACTTCTTCATTTG	1213
Db	5534	CTTCATCTCTTTCTCTCATCTTTGATTTACACCTGGCTTGAGGCTGTCACTTCTTCATTTG	5593
Oy	1214	GTAATCATCTGATCCCAACAGTGGCGGAA-GGTTTGTGGCCACCGTACAGGTATGTCTACG	1272
Db	5594	GTAATCATCTGATCCCAAGTGGCCGAAAGGGAGCTTTGGGCCACGTACAGGTCTGTCTGACA	5653
Oy	1273	CTCACTGCGCAAGCGCATGCGAGAGAAAGTCTGTGTATTAAGAACTTGAAGACTGTGAG	1332
Db	5654	CTTACTGCCAAAGCATAGCAGAGAAAACTGCTTAGTGAAGAACTTAGAAGCTGTGAG	5713
Oy	1333	ACCTTGGGGTCCACATCCACCATCTGCTCCGACAAAGCTGGAATCTGTACATCAGAACCGG	1392
Db	5714	ACCTTGGGGTCCAGTCCACATCTGCTCTGTATTAAGCTGGAATCTGTACATCAGAACCGG	5773
Oy	1393	ATGACAGTGGCTCAGATGGTGTGACATCAATCCATCAAGAGCTGACACCAACAGAGAT	1452
Db	5774	ATGACAGTGGCTCAGATGGTGTGACATCAATCCATCAAGAGCTGATACGACAGAGAT	5833
Oy	1453	CAGAGTGGAGTCTCTTTGACAAAGAGTGAAGCACCCTGGTTTGCTGTCTGCGAATTGCT	1512
Db	5834	CAGAGTGGTGTCTTTTGAACAAGACTTGACGTACTGGCTTGTCTGCGAATTGCA	5893
Oy	1513	GGTCTCTGTAAACAGGGAGAGTGTTCAGGCTAACCAAGAAACCTTGCTATCTTTAAGGCT	1572
Db	5894	GGTCTTTGTAAACAGGGAGAGTGTTCAGGCTAACCAAGAAACCTTACTATTTTAAAGCG	5953
Oy	1573	GCAGTAGCGGAGATGTGTTCCAGATCGGCGCTTTTAAATGTGATGAGAGTCTGCTGTGC	1632
Db	5954	GCAGTGTGAAGAGATGCTCTGTGATCAGCACTCTTAAATGTGATAGAGTGTGCTGTGT	6013
Oy	1633	TCGCTGATGAGATGAGCGAGAAAGTACACCAAGATGTGGAAGTTCCCTTCAACTCCAC	1692
Db	6014	TCGCTGAAGGATGAGAGAAAGATACGCGCAAAATGTGGAAGTACCTTCAACTCCAC	6073
Oy	1693	AACAAATGACAGCTCTCCATTTCAAGAAACCCAAAGCATCGAGGCTTAAGCACTTGCTA	1755
Db	6074	AACAAATGACAGCTGTGTCTATTTCATAGAAACCCAAACACATCGAGGCTCCMAACCTGTGT	6133
Oy	1753	GTGATGAAGGGCGGCCCAAGAAAGATCTTGACCGATGCAAGTTCTATCTCTCCAGCGC	1812
Db	6134	GTGATGAAGGGCGGCCCAAGAAAGATCTTGAACCTTTCAGCTTATCTCTCCAGCGCT	6193
Oy	1813	AAGAGCGAGCCCTCGAGACGAAAGCTGAAGAGCGCTTCAAGATGGCTAGAGCTG	1872
Db	6194	AAGAGCGAGCCCTCGAGATAGAGAGCTGAAGAGCGCTTTCAGAGCGCTTATTTGAGAGCTG	6253

QY 1293 GA-GGAGAACTGCTGTGTGAGAACCTGGAGCTGTGGAGACCTTGGGGTCCACATCCA 13

QY 2372 TGGCTGTACAGGGGATGTGTCATGACTTCCAGCTTGGAAAAGGCAGATATTCGGC 243

D	b		TCCGAGCCCCAGACTCGCTCTCCGCACTGCACATCAGAAACCCTTTGAAGA CTCGGAA	847
O	y	960	CATTGCCCTTCTTCACAACCAACTGTGTGAAGAACTGCACGCTGCATCGTTGTATCAC	1019
D	b	848	CATCACCTTCTTTTCCAACCACTTTGTGAAGAGCAAGCGCTCGGCGCGTGTTGGTGCAC	907
O	y	1020	TGGGATATGCACCCGTGATATGGCAGGATCGCCACCCTTGCTCTT3GGCTTGAAGGCGGCT	1079
D	b	908	GCGGCAACCGCACTGTCAATGGGCGCATATCCCAACCCGGGATCAGGGCTTGAAGGTGGCAA	967
O	y	1080	GACCCCATTGTGTGAAGAAATGAGACACTTCATCCACCTCATCAGCGAGTGGCCGCTGT	1139
D	b	968	GAGCGCCCATTCGCATACGAAATTAAGCACTTATCCAGCTCATACCGGCGGTGTCTT	1027
O	y	1140	CCTGGGAGTGTCTTCTTCTCATTTCTCTCTGTATCCTTAGTACACCTGGCTCGAGGCTGT	1199
D	b	1028	CCTGGGAGTGTCTCTCTTCTCATCTCTCCCTCATTTCTCGAATACCTGGCTTGAAGCTGT	1087
O	y	1200	CATCTTCTCATATGTATATATGTATGCCCAAGCGCCGAAAGTTTGTGGCCACCGTAC	1259
D	b	1088	CATCTTCTCATATCGGATATATGTGGCCAAATGTCCAGAGGCTCTGTGCACCTGTAC	1147
O	y	1260	GGTATGTCTGACGCTCACTGCCAAGCGCATGGCGGAGAAAGAACTGCTGTGTGAAGAACT	1319
D	b	1148	TGTGTGTCTGAAGCTGACCGCCCAAGCGCATGGCCCGAAAGAACTGTGCTGTGTGAAGAACT	1207
O	y	1320	GGAAGCTGTGAGACTTGGGGTCCCATCCACATCTGTCCGACAAAGCTGGAACTCT	1379
D	b	1208	GAAAGCTGTGAAGAACTTGGGGTCCCATCCACATCTGTCCGACAAAGCTGGAACTCT	1267
O	y	1380	GACTCAGAAACCGGATGACAGTGGGCTCACATGTGTGTGACAAATCCATCATAAGCTGA	1439
D	b	1268	CACCTAGAAACCGGATGACAGTGGGCTCACATGTGTGTGACAAATCCATCATAAGCTGA	1327
O	y	1440	CACCAAGAGATCAGATGTTGGGCTCTCTCTTTGACAAAGACGTACGCCACCCTGTGGCTCT	1499
D	b	1328	CACCAAGAGATCAGATGTTGGGCTCTCTCTTTGACAAAGACGTACGCCACCCTGTGGCTCT	1387
O	y	1500	GTTCCAGAAAT - GCTGGCTCTGTGTACAGGGCAGTGTTCAGGCTTAACCAAGAAAACCTG	1557
D	b	1388	GTTTGACATCGCTGGGGTTTTGCCATTCGCCCTGTCTTCAAGGGTGTGAGACATATC	1447
O	y	1558	CCTATCTTAACTGTACGTATGACGGAGATGTTCCGATGCGGCGCTTTAAAGTCATC	1617
D	b	1448	CCTGTGCTCAAGAGGATGTGGCTGGGGAGTCCCTGTGAGCTCTGCCCTGTCAAGTGCATC	1507
O	y	1618	GAGGCTGTGTGGGCTCCGATGAGAGATGAGGAGAAAGTACCAAGATATAGTGGACATT	1677
D	b	1508	GAGGCTGTGTGGGCTCCGATGAGAGATGAGGAGAAAGTACCAAGATATAGTGGACATT	1567
O	y	1678	CCCTTCACTCACAACCAAGTACAGACTCTCCATTCACAAGAACCCMAACGCATCGAG	1737
D	b	1568	CCCTTCAATTCACAACCAAGTACAGACTCTCCATTCACAAGAACCCMAACGCATCGAG	1627
O	y	1738	CCTAAGCACTGTATGATGAAGGGCGCCCAAGAAAGATCTGTGAACGATGAGATTCT	1797
D	b	1628	AACCGATACCTGTGTGATGAAGGGGCGCCCAAGGCAATCTGTGAACGATGAGATTCT	1687
O	y	1798	ATCTCTCTCCACGGCAAGGAGCAGCCCTTGAGAGAAAGCTGTAAGAGACGCTTTCAGAAAT	1857
D	b	1688	ATCTCTCTCAAGGCAAGGAGCAGCCCTTGAGAGAAAGCTGTAAGAGAGGCTTTCAGAAAT	1747
O	y	1858	GCTTACTTGAAGTGTGGGGGCTTTGAGAGACGTGTAGTTTCTTCCACCTCTCTGT	1917
D	b	1748	GCTTACTTGAAGTGTGGGGGCTTTGAGAGACGTGTAGTTTCTTCCACCTCTCTGT	1807
O	y	1918	CTGACGAAACAGTTTCCCGAAGCTTCCAGTTTGACACTATGAAGTCAATTTTCCCGGT	1977
D	b	1808	CTGACGAAACAGTTTCCCGAAGCTTCCAGTTTGACACTATGAAGTCAATTTTCCCGGT	1867
O	y	1978	GATTAAGTGTGTGTGTGTGTATTTATTTCAATGAACCTTCTCGAAGTGTGTGTGT	2037

Db	1868	GACAACTCTGCTTTTGTS63CCTAATGTCATGATCG6CCCAACCCCG69ZAGCCGTCCCT	1927
Qy	2038	GATGCTGTGGGCAAAATGCGGCAGCGCTGGGATTAAAGTCATCATGTGTCAACAGAGACCAT	2097
Db	1928	GAGCGGTGTGGCAAGGTGTGCGACGCGAGGCATCAAGGTGTCATATGTGTACCG9GACATCAC	1987
Qy	2098	CGAATCAACCCAAAGCCAAATGTGTAAAGGGGGGTGG6CATTTATCTCAGAAAGTAAACGACAC	2157
Db	1988	CCATCAACG6CCAAAGG6CATTGTCCAAAGGTGTGG6CATCATCTTTGAAG6GCAACGACACT	2047
Qy	2158	GTGGAAACATTGCTGCCCCGCTCAACATTTCCAGTGAACAGGTGAACCCCAAGATG6C	2217
Db	2048	GTGGAGACATTCGCCCCGCGCTCAACATTTCCCGTCACGAG3TTAACTCCCTGG3AAT9CT	2107
Qy	2218	AAAGCCCTGTAGTAAATATGGCACTGACTTTGAAAGACATTAACCTCTGAGAGACTG9ATGAC	2277
Db	2108	AAAGCCCTGTGTATCCACG6CACG6CTCCAAAG6ACTTCACTCCGAGCAAAATGAGAGAG	2167
Qy	2278	ATTTCGGGTACACACAGAGATTTGTTTGTGTAG6CCTCTCTCAACAGAACTCATC	2337
Db	2168	ATCTCGAAGAAATCAACCCAGATCGTCTTTCG6CCGACATCTCCCTCCAGAAACTCATC	2227
Qy	2338	ATTGTGAGG6CTGTCCAGCG6CAGG6GTG6CATCTGTGCTGTACAGGG6AATGTGTCAAT	2397
Db	2228	ATTGTGAGG6GCTGTCAAGACAGG6GTGTCAATTGTGCTGTGAACGG6AATGTGTGAAC	2287
Qy	2398	GACTCTCCAGCTTTTGA AAAAGGACAGATTTTGG6GTTTGCATG6G6AATGTGTGCTCGAT	2457
Db	2288	GACTCCCCCTCTGAAGAAAGGCGCATTTGG6GTGGCCATGT99CATGT99CTTTGAC	2347
Qy	2458	GTGTCCAGCAAGCTGTCTGCATGATTTCTTTGTGATGACAACTTTGCTCCATGTGACT	2517
Db	2348	GTCTCCAGACAGCGAGCTGTCAATGATCTGTGT9AGACAACTTTGTGCTGTATGTATCA	2407
Qy	2518	GGAGTGAAGAAAGGTGCTGTGATTTATTTGAATTAATTGAAGAAATTCATTTACTTACCCCTA	2577
Db	2408	GGGTTGAGAGAGG6CG6CTGTGATCTTCTGCAACCATAAAGATTCATTTGCTTACACCTGT	2467
Qy	2578	ACAAGTAAACATTTCCGGAATCAACCCCTTCTGTATTTATTTATTTGCAAACTTCACTG	2637
Db	2468	ACGAGCAATATCCCGGAGATCAACGCCCTTCTGTGTTTCATGATG6CCAAACTCCGCTGT	2527
Qy	2638	CCCCGG6GCAACGGTGAACATCTCTGTGATTTGAATTGT99CACTGACATG9TTCG6CCTAT	2697
Db	2528	CCCCGG6GCAATCACTATCTCTGTGATCTGTGATCTGTG6GCACTGACATG6TCCCTGCATC	2587
Qy	2698	TCTGTGGCTATGAACAGGCTGAAAGTGAATCATGATGAAGGCAAGCCAGAAATCCCAA	2757
Db	2588	TCACTGGGTATCGAGGCTGTGCGAAAGGACATCATGAAGACACCCAGAAACCCGCGG	2647
Qy	2758	ACGACAAACTTTGTGAACGAGGCTGTGATCAGATG6CCTAATG6ACAGATCGTATGATC	2817
Db	2648	ACGACAAATTTGTCAATGTAGAACATCATGAGATG6CTTACGG6GAGATTTGAAATGATC	2707
Qy	2818	CAGG6CCTG6GAGGCTTCTTCACTATTTTGTGATTTCTG6GTGAGAACGGTTTCTGTGCC	2877
Db	2708	CAGGCTCTCG6TGGCTTCTTCTTACTTTGTGATCTGTGATCTGTG6CAAAAATGGCTTCTTGGCC	2767
Qy	2878	TTTCACTGTTGG6CATCTCGAGAGACTGTG6ATGACCTGTGATTAATGATGT99AG9AC	2937
Db	2768	GGCAACCTGTGTGG6CATCTCG6CTGMACTGTG6ATGACCG6ACCGTCAMATGACTGTGAAGAC	2827
Qy	2938	AGCTACGG6GAGAGTGTGACCTACAG6ACAGAGAAATTTGTGAGTTTCACTGTG6ACAG	2997
Db	2828	AGTTTACGG6GAGAGTGTGACATTAAGACAGAGAAAGTGTGTGAAGTTTCACTGTG6ACAG	2887
Qy	2998	GCCTTCTTTGTCAGTATCTGTGTATGTG6CACTG6GCTGACTTGTGATCTGTGCAAGACAG	3057
Db	2888	GCCTTCTTTGTGACATCTGTGTGTGTCATGATGTG6GCGCATCTCATATCTGTGCAAGACCGG	2947
Qy	3058	AGGAATGTGCTTTCAGAGAGGG6AATGAATAACAATCTTAAATATTTG6CCTCTTTGAA	3117
Db	2948	AGGAATCTGTGCTTTCAGAGAGG6CATTAAGAAACAATCTGTATCTTTGG6CTGTTTGA6	3007

361 GACGACCATAAACTCAGCTTGATGAATCCATCGTAAATACGGAACAGATTGAGCCGA 420

Db 361 GAGGACCAATAACTCAGCCTGATGATCACTGTAATAACGAAACAGATTGAGCCGA 420
QY 421 GGCGCTAACGCCGCAAGGGCGCTGAGATCTCTGGCTCGGGATGGCCCGCAAGCGCCCTCAG 480
Db 421 GGCTTAACACCGGAAAGGCGCTGAGATCTCTGGCTCGGGATGGCCCGCAAGCGCCCTCAG 480
QY 481 CCCCTCCCACTACTCCCGAGTGGGTCAAAATCTGTGCGAGCTGTGTGGCTTCTCC 540
Db 481 CCCCTCCCACTACTCCCGAGTGGGTCAAAATCTGTGCGAGCTGTGTGGCTTCTCC 540
QY 541 ATGTACTGTGATGAGGACATCTTTGTTCTTGCTTATGGATCCGAAGTCTCTACA 600
Db 541 ATGTACTGTGATGAGGACATCTTTGTTCTTGCTTATGGATCCGAAGTCTCTACA 600
QY 601 GAAGAGAACCAACAATGATGATCTGATCTGCGGGGTGCTGCGTGTGCTGTCTATC 660
Db 601 GAAGAGAACCAACAATGATGATCTGATCTGCGGGGTGCTGCGTGTGCTGTCTATC 660
QY 661 ATTAAGCTGCTGTTCTCTATTAATCAAGAAAGCAAAAAGCTCCAAATCATGAAATCCTTC 720
Db 661 ATTAAGCTGCTGTTCTCTATTAATCAAGAAAGCAAAAAGCTCCAAATCATGAAATCCTTC 720
QY 721 AAGAAATGCTCTCTCAAGCAAGCGCTGTGATTTGAAATGAAAGAAAGATGACATTAAC 780
Db 721 AAGAAATGCTCTCTCAAGCAAGCGCTGTGATTTGAAATGAAAGAAAGATGACATTAAC 780
QY 781 GCGAGAGATGCTGCTGATGATCTGATCTGATGAGGAGAGAGCGGATCCCTGCT 840
Db 781 GCGAGAGATGCTGCTGATGATCTGATCTGATGAGGAGAGAGCGGATCCCTGCT 840
QY 841 GATTTTAAATATATTTTAAATGCTGAAAGTATTAATCTGATCTGATCTGATGAA 900
Db 841 GATTTTAAATATATTTTAAATGCTGAAAGTATTAATCTGATCTGATCTGATGAA 900
QY 901 TTAGAAGCCCGAGATGAGTCCCGGATTTTCAAGAAAGCAAGCCCGTGGAGACAGGAAAC 960
Db 901 TTAGAAGCCCGAGATGAGTCCCGGATTTTCAAGAAAGCAAGCCCGTGGAGACAGGAAAC 960
QY 961 ATTGCTTCTTCTCAACCAACTGTGTGAAGAAAGTGCAGCTGCTGTGTGTAACCT 1020
Db 961 ATTGCTTCTTCTCAACCAACTGTGTGAAGAAAGTGCAGCTGCTGTGTGTAACCT 1020
QY 1021 GGGGATGAGACCTGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAG 1080
Db 1021 GGGGATGAGACCTGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAG 1080
QY 1081 ACCCGCATTTGTAAGAAATGAGAGACCTCATCACTCAAGGGGTGAGCGCTGTC 1140
Db 1081 ACCCGCATTTGTAAGAAATGAGAGACCTCATCACTCAAGGGGTGAGCGCTGTC 1140
QY 1141 CTGGGGGTGCTTTCTTCTTCTCTCTCTGATCTCTGATCACTGCTGAGGCTGTC 1200
Db 1141 CTGGGGGTGCTTTCTTCTTCTCTCTCTGATCTCTGATCACTGCTGAGGCTGTC 1200
QY 1201 AATTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 AATTCCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 GATATGCTGACGCTCACTGCGCAAGCGGATGCGAGAAAGATGCGTGTGAAGAACTG 1320
Db 1261 GATATGCTGACGCTCACTGCGCAAGCGGATGCGAGAAAGATGCGTGTGAAGAACTG 1320
QY 1321 GAAAGCTGTGAGAGCTTTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1380
Db 1321 GAAAGCTGTGAGAGCTTTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1380
QY 1381 ACTCAGAACCGAGATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 ACTCAGAACCGAGATGACAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 AATTAAGATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
Db 1441 AATTAAGATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500

QY 1501 TCCAGATTTGCTGCTCTGTAAACAGGAGGATGTTTCAAGCTTAACCAAGAAACCTGCT 1560
Db 1501 TCCAGATTTGCTGCTCTGTAAACAGGAGGATGTTTCAAGCTTAACCAAGAAACCTGCT 1560
QY 1561 ATTCCTTAAGCGTGCAGTACCGGAGATGCTTCCAGTGTGCGGCTCTTTAAAGTGCATCGAG 1620
Db 1561 ATTCCTTAAGCGTGCAGTACCGGAGATGCTTCCAGTGTGCGGCTCTTTAAAGTGCATCGAG 1620
QY 1621 GTCTGCTGTGCTGCTGATGAGATGAGAGGAGATGAGATGAGATGAGATGAGATGAG 1680
Db 1621 GTCTGCTGTGCTGCTGATGAGATGAGAGGAGATGAGATGAGATGAGATGAGATGAG 1680
QY 1681 TTCATCTCAGCAACAAGTACAGCTCTCCATTCACAAAGCCCAAGCGATGAGAGCT 1740
Db 1681 TTCATCTCAGCAACAAGTACAGCTCTCCATTCACAAAGCCCAAGCGATGAGAGCT 1740
QY 1741 AAGCAGCTGCTAGTATGAGAGGCGCCCAAGAAAGATCCTGAGCCGATGCACTTATC 1800
Db 1741 AAGCAGCTGCTAGTATGAGAGGCGCCCAAGAAAGATCCTGAGCCGATGCACTTATC 1800
QY 1801 CTCTCAGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 CTCTCAGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 TACCTAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db 1861 TACCTAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
QY 1921 GAGGACAGTTTCCCGAAGGCTTCCAGTTTGAACAGTATGAGTAAATTTTCCCGTGGAT 1980
Db 1921 GAGGACAGTTTCCCGAAGGCTTCCAGTTTGAACAGTATGAGTAAATTTTCCCGTGGAT 1980
QY 1981 AACCTCTGCTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db 1981 AACCTCTGCTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
QY 2041 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Db 2041 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
QY 2101 ATACAGGCGAAAGCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Db 2101 ATACAGGCGAAAGCGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
QY 2161 GAGGACATTTGCTGCGGCTCAACATTTCCAGTGAACAGGTGAACCCAGAGATGCGCAG 2220
Db 2161 GAGGACATTTGCTGCGGCTCAACATTTCCAGTGAACAGGTGAACCCAGAGATGCGCAG 2220
QY 2221 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
Db 2221 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
QY 2281 TACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db 2281 TACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
QY 2341 GTGAGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
Db 2341 GTGAGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
QY 2401 TCTCCAGCTTTGAAAAGGAGATTTGGGGTTGCGATGGGATTTGTTGGCTGGGATG 2460
Db 2401 TCTCCAGCTTTGAAAAGGAGATTTGGGGTTGCGATGGGATTTGTTGGCTGGGATG 2460
QY 2461 TCCAGAGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2461 TCCAGAGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
QY 2521 GTAGAGAGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 2521 GTAGAGAGAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580

2581 AGTACATTTCCGGAATACCCCTTCTTGAATATTATTATTCGAAACATTCGACTGCC 2640
2581 AGTACATTTCCGGAATACCCCTTCTTGAATATTATTATTCGAAACATTCGACTGCC 2640
2641 CTGGGACCCGTCACCATCTCTGCACTTGAATCTTGGGCACTGACATGGTCCGCCATCTCT 2700
2641 CTGGGACCCGTCACCATCTCTGCACTTGAATCTTGGGCACTGACATGGTCCGCCATCTCT 2700
2701 CTGGGCTATGAAACAGCTGAAAGTACATCATGAAAGAGCAGCCGAAATCCGAAACG 2760
2701 CTGGGCTATGAAACAGCTGAAAGTACATCATGAAAGAGCAGCCGAAATCCGAAACG 2760
2761 CTGGGCTATGAAACAGCTGAAAGTACATCATGAAAGAGCAGCCGAAATCCGAAACG 2820
2761 GACAAACCTTGCAACAGAGCTGATCAGCATGAGCTGATGCAATGATGATGATCCAG 2820
2821 GGCCTGGGAGGCTCTTCTTCACTATTATTTGATTTCTGCTGAGAAAGCTTCTGCCCTTT 2880
2821 GGCCTGGGAGGCTCTTCTTCACTATTATTTGATTTCTGCTGAGAAAGCTTCTGCCCTTT 2880
2881 CACCTGTTGGGACATCCGAGAGACCTGGGATGACCGCTGATTAATGATGTGAGAGACG 2940
2881 CACCTGTTGGGACATCCGAGAGACCTGGGATGACCGCTGATTAATGATGTGAGAGACG 2940
2941 TACGGGACAGAGTGAACCTTACGAGAGAGAGAGATTTGAGATTCACTGCGACAGCGCC 3000
2941 TACGGGACAGAGTGAACCTTACGAGAGAGAGAGATTTGAGATTCACTGCGACAGCGCC 3000
3001 TTCTTTGTCAGTATCGTGTAGTGTGAGAGGCTGACCTTGGTCACTGCAAGACGAGAAAG 3060
3001 TTCTTTGTCAGTATCGTGTAGTGTGAGAGGCTGACCTTGGTCACTGCAAGACGAGAAAG 3060
3061 AATTCTGTCTTCCAG 3120
3061 AATTCTGTCTTCCAG 3120
3121 ACAGCTCTTGCTGCTTCTCTGCTCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 3180
3121 ACAGCTCTTGCTGCTTCTCTGCTCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 3180
3181 CCCCCTAAACCTTACTTGT 3240
3181 CCCCCTAAACCTTACTTGT 3240
3241 GACGAGGTGGAGAGCTCATCATCAGGCGAGCGCTGCGGCTGCGGCTGCGGCTGCGGCT 3300
3241 GACGAGGTGGAGAGCTCATCATCAGGCGAGCGCTGCGGCTGCGGCTGCGGCTGCGGCT 3300
3301 TACTACTAGCCCACTGCGCTGCAAGCGCTGCAAGCATGTGTGCACTGCACTGCACTG 3360
3301 TACTACTAGCCCACTGCGCTGCAAGCGCTGCAAGCATGTGTGCACTGCACTGCACTG 3360
3361 TACCCCCCTTTGT 3420
3361 TACCCCCCTTTGT 3420
3421 CCAAGCATGTGGAGATCCAGAGCTCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 3480
3421 CCAAGCATGTGGAGATCCAGAGCTCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 3480
3481 GGGGAGGGCTGCGCGGAG 3540
3481 GGGGAGGGCTGCGCGGAG 3540
3541 CCTTTTGT 3600
3541 CCTTTTGT 3600
3601 GGATTTTACAAATTAAGATGGCTATTATTAACGGA 3636
3601 GGATTTTACAAATTAAGATGGCTATTATTAACGGA 3636
3601 GGATTTTACAAATTAAGATGGCTATTATTAACGGA 3636

RESULT 2
US-09-090-535-5
Sequence 5, Application US/090535A
Patent No. 6309874
GENERAL INFORMATION:
APPLICANT: BELUSA, Roger
TITLE OF INVENTION: SELECTION MARKER
FILE REFERENCE: BELUSA 09/090,535
CURRENT APPLICATION NUMBER: US/09/090,535A
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: US 60/048,601
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 3636
TYPE: DNA
ORGANISM: Rattus rattus
US-09-090-535-5

Query Match 99.7%; Score 3626.4; DB 4; Length 3636;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 3630; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 GGAACCTTCGGGAG 60
1 GGAGCTTCGGGAG 60
61 GCGGACAG 120
61 GCGGACAG 120
121 CAGGCTTATGTTCCGCTCTGAGTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 180
121 CAGGCTTATGTTCCGCTCTGAGTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 180
181 CTCTCTTTTCTAGTCTCCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
181 CTCTCTTTTCTAGTCTCCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
241 GGGAG 300
241 GGGAG 300
301 AAGACAAAG 360
301 AAGACAAAG 360
361 GAGACCAATTAATCTAGGCTGATGATCTCATCTGTAATACGAAACAGATTGAGCCGA 420
361 GAGACCAATTAATCTAGGCTGATGATCTCATCTGTAATACGAAACAGATTGAGCCGA 420
421 GGCCTTAACACCCGCAAG 480
421 GGCCTTAACACCCGCAAG 480
481 CCCCCTCCCACTAATCCGAG 540
481 CCCCCTCCCACTAATCCGAG 540
541 ATGTTACTGTGATGAG 600
541 ATGTTACTGTGATGAG 600
601 GAAAG 660
601 GAAAG 660
661 ATTAAG 720
661 ATTAAG 720
721 AAGACATGATCTCCTCAGCAAGCCCTGATTCGAAATGAGAGAGAGAGAGAGAGAGAG 780

QY 2941 TACGGGACAGCTGAGCCTACGAGCAGAGAAATTGTGAGATTCACTTGCACACAGGCC 3000
Db 2941 TACGGGACAGCTGAGCCTACGAGCAGAGAAATTGTGAGATTCACTTGCACACAGGCC 3000
QY 3001 TTCTTTTGCAGTATCGTGTGATGCGAGTGGGCTGACTTGTCTCTGAAAGCAGAAAG 3060
Db 3001 TTCTTTTGCAGTATCGTGTGATGCGAGTGGGCTGACTTGTCTCTGAAAGCAGAAAG 3060
QY 3061 AATTCTGCTTCACAGCAGGAAATGAAGAACAGATCTTAATATTGTGAGCTTTTGAAGAG 3120
Db 3061 AATTCTGCTTCACAGCAGGAAATGAAGAACAGATCTTAATATTGTGAGCTTTTGAAGAG 3120
QY 3121 ACAGCTCTTGTGCTTCT 3180
Db 3121 ACAGCTCTTGTGCTTCT 3180
QY 3181 CCGCTCAAACTACTGT 3240
Db 3181 CCGCTCAAACTACTGT 3240
QY 3241 GACGAGTGGCAGAGCTCATCATCAGGCGACGCCCTGGCGGCTGGGAGAGAAAGCC 3300
Db 3241 GACGAGTGGCAGAGCTCATCATCAGGCGACGCCCTGGCGGCTGGGAGAGAAAGCC 3300
QY 3301 TACTACTAGCCCACTGCGCTGACGCGGAGAAATTGTGTCACACACTGACCTTACCCC 3360
Db 3301 TACTACTAGCCCACTGCGCTGACGCGGAGAAATTGTGTCACACACTGACCTTACCCC 3360
QY 3361 TACCCCCCTTTGTACTTCACTTCAAGTCTTGGAGCTCGGAACCTTACCTGTGAGAAAGCA 3420
Db 3361 TACCCCCCTTTGTACTTCACTTCAAGTCTTGGAGCTCGGAACCTTACCTGTGAGAAAGCA 3420
QY 3421 CCNAGCATGTGGGATCCGAGCTCTGGAATGAAGCATGTAGCTTAAATGGGGGGCGG 3480
Db 3421 CCNAGCATGTGGGATCCGAGCTCTGGAATGAAGCATGTAGCTTAAATGGGGGGCGG 3480
QY 3481 GGGGAGGCTGCGCCGAAAAACACCGTGGAGCGGAGCGAGCGGGAAGCTTATATGTG 3540
Db 3481 GGGGAGGCTGCGCCGAAAAACACCGTGGAGCGGAGCGAGCGGGAAGCTTATATGTG 3540
QY 3541 CTTTCTTTTGT 3600
Db 3541 CTTTCTTTTGT 3600
QY 3601 GGAATTTTAAATAAAGATGGCTATTATTAACGGA 3636
Db 3601 GGAATTTTAAATAAAGATGGCTATTATTAACGGA 3636

RESULT 3
US-09-090-535-6
Sequence 6, Application US/09090535A
Patent No. 6309874
GENERAL INFORMATION:
APPLICANT: BELUSA, Roger
TITLE OF INVENTION: SELECTION MARKER
FILE REFERENCE: BELUSA 09/090,535
CURRENT APPLICATION NUMBER: US/09/090,535A
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: US 60/048,601
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 3636
TYPE: DNA
ORGANISM: Rattus rattus
US-09-090-535-6

Query Match 99.7%; Score 3626.4; DB 4; Length 3636;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3630; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGAGCTCGCGGAGAGAGAGCGGAGCACTGGGAGCGCGCGGCGGAGCGAGGAGCG 60
Db 1 GGAGCTCGCGGAGAGAGAGCGGAGCACTGGGAGCGCGCGGCGGAGCGAGGAGCG 60
QY 61 GCGGACAGAGCGGCGGCTCGGCTCGGAGGCGCGGCGGCTCTCTCTCTCTCTCTCTCT 120
Db 61 GCGGACAGAGCGGCGGCTCGGCTCGGAGGCGCGGCGGCTCTCTCTCTCTCTCTCTCT 120
QY 121 CAGCCTAGTTCGCGCTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 180
Db 121 CAGCCTAGTTCGCGCTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 180
QY 181 CT 240
Db 181 CT 240
QY 241 GGGAGGGGCTTGAAGAGAGCAAGTATGAGCCGAGCTGTATCAGAACTGAGGAGCAAG 300
Db 241 GGGAGGGGCTTGAAGAGAGCAAGTATGAGCCGAGCTGTATCAGAACTGAGGAGCAAG 300
QY 301 AAGAGCAAGAGGCGAAGAAAGGAAAGGAAATGAGAGCACTCAAGAAAGAAAGTCTATG 360
Db 301 AAGAGCAAGAGGCGAAGAAAGGAAAGGAAATGAGAGCACTCAAGAAAGAAAGTCTATG 360
QY 361 GAGGACCATTAATCTCAGCTGATGAACTCCATCTTAATAGGAAAGAAATTGAGCTTGA 420
Db 361 GAGGACCATTAATCTCAGCTGATGAACTCCATCTTAATAGGAAAGAAATTGAGCTTGA 420
QY 421 GGGCTAACACCCGCGAGGCGGCTGAGATCTCTGCTGGGATGGGCGGCGGCTGAG 480
Db 421 GGGCTAACACCCGCGAGGCGGCTGAGATCTCTGCTGGGATGGGCGGCGGCTGAG 480
QY 481 CCGCTCCGCTACTCCGAGTGGGTCAATCTGTGCGGAGCTTCTGCTGCTCTCTCTCTCT 540
Db 481 CCGCTCCGCTACTCCGAGTGGGTCAATCTGTGCGGAGCTTCTGCTGCTCTCTCTCTCT 540
QY 541 ATGTACTGTGATGGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
Db 541 ATGTACTGTGATGGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
QY 601 GAAGAGAACCAACCAATGATGATCTGTAAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 GAAGAGAACCAACCAATGATGATCTGTAAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 ATAACTGGCTTCT 720
Db 661 ATAACTGGCTTCT 720
QY 721 AAGAACTGGTCCCTCGCAAGGCTCTGTATGGAATGGAAGAAATGAGATGAGATGAGAT 780
Db 721 AAGAACTGGTCCCTCGCAAGGCTCTGTATGGAATGGAAGAAATGAGATGAGATGAGAT 780
QY 781 GCAAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 GCAAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GATCTCAGATCATATCTGCAATATGCTGCAAGTGTGATTAATCTCTCTCTCTCTCTCTCT 900
Db 841 GATCTCAGATCATATCTGCAATATGCTGCAAGTGTGATTAATCTCTCTCTCTCTCTCTCT 900
QY 901 GATCTCAGATCATATCTGCAATATGCTGCAAGTGTGATTAATCTCTCTCTCTCTCTCTCT 960
Db 901 GATCTCAGATCATATCTGCAATATGCTGCAAGTGTGATTAATCTCTCTCTCTCTCTCTCT 960
QY 961 ATGGCTTCTTCTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 ATGGCTTCTTCTCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 GGGGATCGCAGCTGATGAGGAGATGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 GGGGATCGCAGCTGATGAGGAGATGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

Db	3241	GAGCAGGTTGCGGAAAGCTCATCATCAGGCGCAGCGCCCTGCGCGCTGGGTG99AGAAAGGAAMCC	3300
QY	3301	TACTACTAGCCCACTGCTGCTGACGACCGCTG799AAGCATTTGTGTCACACACTGCACTCACTCC	3360
Db	3301	TACTACTAGCCCACTGCTGCTGACGACCGCTG799AAGCATTTGTGTCACACACTGCACTCACTCC	3360
QY	3361	TACCCCCCTTTGTGTGACTCAAGTCGTGGAGTGTGGAACTCAACCTGTGTAGGAAACCA	3420
Db	3361	TACCCCCCTTTGTGTGACTCAAGTCGTGGAGTGTGGAACTCAACCTGTGTAGGAAACCA	3420
QY	3421	CCAAAGCATGTGGGGATTCCTGACCTCTCTG9AAATGAAGCATGTAGCTGTAAATGG9393G93	3480
Db	3421	CCAAAGCATGTGGGGATTCCTGACCTCTCTG9AAATGAAGCATGTAGCTGTAAATGG9393G93	3480
QY	3481	GGGAGGAGGCTGCCCCGAAAAACACCTGTGTGACGGGGACGACAGCGGGGAGCTTTATATATGTG	3540
Db	3481	GGGAGGAGGCTGCCCCGAAAAACACCTGTGTGACGGGGACGACAGCGGGAGCTTTATATATGTG	3540
QY	3541	CCCTTTGTTTTGTATAAAAAAGGAANAACCTGGAAACACGTGAANAAGTTACGTTTTATATCT	3600
Db	3541	CCCTTTGTTTTGTATAAAAAAGGAANAACCTGGAAACACGTGAANAAGTTACGTTTTATATCT	3600
QY	3601	GGATTTTACAATAAAGATGCGCTATTATATACGAA	3636
Db	3601	GGATTTTACAATAAAGATGCGCTATTATATACGAA	3636

```

RESULT 4
US-09-090-535-7
: Sequence 7, Application US/09090535A
: Patent No. 6309874
: GENERAL INFORMATION:
: APPLICANT: BELUSA, Roger
: TITLE OF INVENTION: SELECTION MARKER
: FILE REFERENCE: BELUSA 09/090,535
: CURRENT APPLICATION NUMBER: US/09/090,535A
: CURRENT FILING DATE: 1998-06-04
: EARLIER APPLICATION NUMBER: US 60/048,601
: EARLIER FILING DATE: 1997-06-04
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
:   LENGTH: 3636
:   TYPE: DNA
: ORGANISM: Rattus rattus
: US-09-090-535-7

```

Query Match	99.6%	Score 3621.6	DB 4	Length 3636
Best Local Similarity	99.8%	Pred. No. 0		
Matches 3627	Conservative	0	Mismatches 9	Indels 0
			Gaps	0

[illegible][illegible]

1.6%; Score 57.2; DB 3; Length 5421;

2292 CACGAGATTGTTGCTAGGACCTCTGCTCACACAGAAGCTCATCATTTGTGGAGGGCTG 2351


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; Sequence 18, Application US/09041866
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Breziden, Dale E.
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; NUMBER OF SEQUENCES: 72
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,866
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 163..4099
US-09-041-866-18

Query Match          1.3%; Score 49; DB 4; Length 4481;
Best Local Similarity 51.6%; Pred. No. 0.0082;
Matches 112; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY      31 GCAGCGGGGCGGCGGACGAGCAGCGGCGGCGAGCGAGCGAGCGCTCGGTCCGGGAGC 90
DB      660 GCAGCGAGCAGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 719
QY      91 GCCGCAGCTCCCTCCCTCTTCTTCGCCGAGGAGCCCTAGTTCCCGCCTCTCGACTCCCC 150
DB      720 GCAGCGCGCGCGCGCGGCTGCAATGTCGCAAC3CCCGGCGCACGCGCTTCTTAGCGTC 779
QY      151 GGCTCACTCTTCCCAGCCGCGGAGCGTCTCTCTTCTTAGTGTCACGACAGGAGC 210
DB      780 GCCGCGCGCGCGCTTGC CGCGCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 839
QY      211 CGGCGCGGCGCGCGGAGCGCGCGCGCACCATGAGGAAG 247
DB      840 CTCCTCGGTGTCGGCGGACCTCGGCGCGCGGAGG 876

RESULT 15
US-08-118-200-1
; Sequence 1, Application US/08118200
; Patent No. 6197500
; GENERAL INFORMATION:
; APPLICANT: SUTHERLAND, Grant R
; APPLICANT: RICHARDS, Robert I
; APPLICANT: SCHLESSINGER, David
; APPLICANT: NAGARAUA, Ramalah

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Query Match	36.3%	Score 1320.4	DB 10	Length 1338
Best Local Similarity	99.2%	Pred. No. 0	Mismatches 11	Indels 0
Matches 1337	Conservative	0		Gaps
QY 1222	GTGAGCCACGTCGCGGAAAGTTTGCTGGCGCACCGTCACCGGATGTGTCGACGCTCACTGCC	1281		
Db 1	GTAGCCACACTGCGGAAAGTTTGCTGGCGCACCGTCACCGATGTGTCGACGCTCACTGCC	60		
QY 1282	AAGCGCATGGCGAGAGAAAGATCGCCCTGTGGAGAAACCTGGAGCTGTGGAGACCTTGGG	1341		
Db 61	AAGGCGATGGCGCGAGAAAGATCGCCCTGTGGAGAACCTGGAAAGCTGTGGAGACCTTGGG	120		
QY 1342	TCCACATCCACCACTCTGCTCCGACCAAGACTGGAATCTGACTCAGAACCGGATGACAGT	1401		
Db 121	TCCACATCCACCACTCTGCTCCGACCAAGACTGGAATCTGACTCAGAACCGGATGACAGT	180		
QY 1402	GCTCACAATGTGTTTGAACATCAATTCATGAAAGTGCAGACCCACAGAGATACAGATGGG	1461		
Db 181	GCTCACAATGTGTTTGAACATCAATTCATGAAAGTGCAGACCCACAGAGATACAGAGTGG	240		

[illegible][illegible][illegible]

QY 2662 TCCATTGACCTGGACCTGACATGCTTCCGCCATCTCTGCTCTATGACAGGCTGAA 2721
 Db 619 TCCATTGACCTGGACCTGACATGCTTCCGCCATCTCTGCTCTATGACAGGCTGAG 678
 QY 2722 AGTGACATCATGAAAGAGCGCCAGCAAAATCCCAAAACGAAACTGTGAGAGGAGCT 2781
 Db 679 AGTGACATCATGAAAGAGCGCCAGCAAAATCCCAAAACGAAACTGTGAGAGGAG 738
 QY 2782 CTGATCAGCATGAGCTATGAGACAGATCGATATGATCCAGGCGCTGGAGGCTTCTGACT 2841
 Db 739 CTGATCAGCATGAGCTATGAGACAGATCGATATGATCCAGGCGCTGGAGGCTTCTGACT 798
 QY 2842 TATTTTGTGATTTCTGCTGAGAACGTTTCTGCTTCACTGTTGGGATCCGAGAG 2901
 Db 799 TACTTTGTGATTTCTGCTGAGAACGTTTCTGCTTCACTGTTGGGATCCGAGAGT 858
 QY 2902 ACCTGAGATGAGCTGAGTGAATGATGATGAGAGACAGTACGAGGAGCAGTGAAGCTTAC 2961
 Db 859 GACTGGATGACCGCTGATGATCAAGATGTGAGAGACAGTACGAGGAGCAGTGAAGCTTAC 918
 QY 2962 GAGCAGAGAGAGATTTGAGAGTGTACCTGCTACAGGCTTCTTGTGATGATGCTGTA 3021
 Db 919 GAGCAGAGAGAGATTTGAGAGTGTACCTGCTACAGGCTTCTTGTGATGATGCTGTA 978
 QY 3022 GTGCAAGTGGGCTGACTGATCTGCAAGACAGAGAGATTTCTGCTTCAAGAGAGGA 3081
 Db 979 GTGCAAGTGGGCTGACTGATCTGCAAGACAGAGAGATTTCTGCTTCAAGAGAGGA 1038
 QY 3082 ATGAGAGAGAGATTTGATTTTGGCTCTTTGAGAGAGAGCTTGTGCTGCTTCTG 3141
 Db 1039 ATGAGAGAGAGATTTGATTTTGGCTCTTTGAGAGAGAGCTTGTGCTGCTTCTG 1098
 QY 3142 TCTTACTGCTTGGATGAGTGTGAGAGCTTGAAGATGATCCCTCAAACTACTGTTGG 3201
 Db 1099 T----- 1099
 QY 3202 TTCTGTGCTTCCCTACT 3261
 Db 1100 -----CTTACT 1146
 QY 3262 ATGAGAGAGAGCTTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3321
 Db 1147 ATGAGAGAGAGCTTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
 QY 3322 CAGCCCGTGAACATTTGAG 3378
 Db 1207 CAGCCCGTGAACATTTGAG 1266
 QY 3379 TTCAAGTCTTGAAGCTGAGAGCTTACCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAG 3437
 Db 1267 TTC-AGTCTTGAAGTGTGAGAGCTTACCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
 QY 3438 CCAGAGCTTCTGAGAGTGAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3497
 Db 1326 CAGAGAGCTTCTGAGAGTGAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1385
 QY 3498 AAACAGCTTGAAG 3557
 Db 1386 ACCATCATCTGTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1445
 QY 3558 AAAAG 3617
 Db 1446 AAAAG 1505
 QY 3618 GATGGCTATTATACGAGAA 3636
 Db 1506 GATGGCTATTATATGAGAA 1524

RESULT 3
 US-09-870-472-9
 Sequence 9, Application US/09870472
 Patent No. US060095023A1

; GENERAL INFORMATION:
 ; APPLICANT: LEE, Kyunglin et al.
 ; TITLE OF INVENTION: Ige-dependent histamine-releasing factor (HRF) receptor, HRF-
 ; TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
 ; TITLE OF INVENTION: thereof
 ; FILE REFERENCE: 1599-0198P
 ; CURRENT APPLICATION NUMBER: US/09/870,472
 ; CURRENT FILING DATE: 2001-06-01
 ; PRIORITY APPLICATION NUMBER: KR10-2000-0030130
 ; PRIORITY FILING DATE: 2000-06-01
 ; SOFTWARE: KOPATIN 1.71
 ; SEQ ID NO 9
 ; LENGTH: 1338
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 ; US-09-870-472-9
 Query Match 23.9%; Score 970 3; DB 10; Length 1338;
 Best Local Similarity 78.2%; Pred. No. 3; Se-217;
 Matches 1046; Conservative 0; Mismatches 292; Indels 0; Gaps 0;
 QY 1222 GTAGCCAACTGCGGAGAGGTTTCTGCGCCACGTCACGATGCTGACGCTCACTGCC 1281
 Db 1 GTGGCCAAATGCCAGAGGGGCTGCTGCTACTGTACGAGTGTCTGACGCTGACCCGC 60
 QY 1282 AAGGCATGCGGAGAGAGAACTGCTGCTGAGAGAACTGAGAGCTGTGAGAGACCTTGAGGG 1341
 Db 61 AAGGCATGCGCTGAGAGAACTGTCTGTAAAGAACTGTGAGAGCGGTGAGAGCGCTAGAGC 120
 QY 1342 TCCACATCAGCATCTGCTCCGACAGAGCTGAACTCTGACTCAGAAACCGATGACAGT 1401
 Db 121 TCCACATCAGCATCTGCTCCGACAGAGCGGACACCTTACCCAAACCGATGACAGT 180
 QY 1402 GCTCAGATGCTGTTGACAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1461
 Db 181 GCTCAGATGCTGTTGACAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 240
 QY 1462 GTCTCTTGTGACAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
 Db 241 ACCTCTTGTGACAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 1522 AACAGAGAGAGTGTTCAG 1581
 Db 301 AACAGAGAGAGTGTTCAG 360
 QY 1582 GAGAGAGAGAGTGTTCAG 1641
 Db 361 GAGAGAGAGAGTGTTCAG 420
 QY 1642 GAGATGAGAGAGAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1701
 Db 421 GAGATGAGAGAGAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 1702 CAGCTCTCATTCAAG 1761
 Db 481 CAGCTCTCATTCAAG 540
 QY 1762 GAG 1821
 Db 541 GAG 600
 QY 1822 CCGCTGAG 1881
 Db 601 CCGCTGAG 660
 QY 1882 GAG 1941
 Db 661 GAG 720
 QY 1942 TTGCAATTTGACATGATGAG 2001
 Db 721 TTGCAATTTGACATGATGAG 780

Query Match 23.2%; Score 844.4; DB 10; Length 1338;
Best Local Similarity 76.9%; Freq. No. 2,76-210,
Matches 1028; Conservative 0; Mismatches 309; Indels 0; Gaps 0;

1232 GTAGCTAAATTGAGGGAATTTTGTGGTCAACCGGTCAAGGTAATGTCCTACGCTCAGCTGC 1281

[illegible]

Query	Match	Similarity	Score	DB	Length
Best Local	Similarity	75.7%	Pred. No.166-193;		
Matches 1026;	Conservative	0;	Mismatches 312;	Indels 17;	Gaps 5

QY	1222	GTAGCCAAACGTCCTCCGGAAAGTTTGCTGAGCCACCGCTGACAGATAATGTCATGACGCTCACTG9CC	1281
Db	1	GTGGCCAAAGTCCCTGAGGGGGCTTCTGGCCACTGTCAGTGTGTGCTGTAGACCCGTGACAGCC	60
QY	1283	AAGCGATGGCGAGGAAGAACTGGCTGTGTGAAGAACCTTGGAAGCTGTGAGACCTTGGGG	1341
Db	61	AAGCGATGGCGAGGAAGAACTGGCTGTGTGAAGAACCTTGAGAGCGGTGTGAGACGCTGGGCC	120
QY	1342	TCCACATCCACCATCTGCTCTCCGACAGAGACTGMAACTCTGATCAGAAACCGGATGACAGG	1401
Db	121	TCCACCTCCACCATCTGCTCTCCGACAAAGAGGAGACCTTACCCAGAAACCGATGACCGCTC	180
QY	1402	GCTCAGTGTGGTTTACATCAATTCATGAAAGCTGAGACCAACAGATCAGAGTGGG	1461
Db	181	GCCCATGTGTGTCCACAAACCAATTCATGAGGCTGACACACCGAAGATCAGTGTGGG	240
QY	1462	GTCTCCTTTGACAAAGAGCTGAGCGACCTGTGCTGTGTCCAGAAATTGTGTGTCTGT	1521
Db	241	GCCACTTTTGACAAAGAGATCCCTACGTGAGCGCCCTGTCTGGAATTTGTGTGTCTGTG	300
QY	1522	AACAGGAGAGTGTTTTAAAGGTAAACCAAGAAACCTGTGCTATCTCTTAAAGGTGAGATAGCG	1581
Db	301	AACGAGAGAGTGTTTTAAAGGTAAAGGACAGAGAAACATCTTCGTGTAAAGGAGACAGCT	360

Oy	1582	GGAGATGCTTCCGAGTCGGCGGCTCTTAAAGTGCATCGAAGTTCCTGAGCTCGGTATG	164
Db	361	GGTATGCTCTTGAAGTCAGCTTGTCTCAAGTGTCTAGCTCTCTGTGGTCAGTGAGG	420
Oy	1642	GAGATGAGGAGAGATGACCAAGATAGTGAGATTCCTCTTAACCTCCACCACAACTAC	1701
Db	421	AAATGAGAGACAGAAACCCTCAAGGTGGAGATTCCTTCAACTGTACCAACAAATAC	480
Oy	1702	CAGGTCCCATTCACAGAAACCCAAACGATGGAGCTTAAAGCTTAAAGCTAGTATAG	1761
Db	481	CAGGTGCTATCCACAGCGAGAGAGACAGACCCTCCAGACCNNNAAGTGTGTATAG	540
Oy	1762	GGCGCCCCAGAAAGATCTGTGACCCGATGCACTTATCTCTCTCCACGCGAAGACAG	1821
Db	541	GGGGCCCCAGAGGCACTTCTGAGCCGATGCTCACATCTCTGTGCAAGGCGAAGATC	600
Oy	1822	CCCTGACCAAGAAAGCTGAAAGACGCTCTTCAAGATGCTTCAAGCTGGGAGGCTT	1881
Db	601	CCGTGACACAGAGATGCAAGTGTCTTTCAAAATGCTTACATGAGACTGGGAGACTT	660
Oy	1882	GGAAGGCTGTAGATTCTTCCACACTCTTCTGTCCCTGACGAACAGTTTCCGAAGGC	1941
Db	661	GGGAGGCTGTGCTGGGATTTCTGTCAACTGATCTGCATCTGMAAATTTCTCTGAGGC	720
Oy	1942	TTCCAGTTTACACTGATGAAAGCATTTCCCGGAGATACCTCTGTTGTGGTGT	2001
Db	721	TTCAAAATTGACACGAGATGCTGAACCTTCCACGAGAACCTTTGCTTTGTAGAGCTC	780
Oy	2002	ATCTCCATGATTGACCTCTCTGAGCTGTCTTCCCGATGTGTGGAGCAAAATGCTCGACG	2061
Db	781	ATGTCTATGATTGACCTCTCCCGGCTGCTGTGGCCAGATGCTGTGGGCAAGTGTCTGAAGC	840
Oy	2062	GCTGGGATTAAAGTCATCAAGGTCAAGAGACATCTCAATACAGCCAAAGCCATTGCT	2121
Db	841	GCAGCATCAAGGATCATAGTGTACCGGGATCACCTTATCAGACCCAAAGCCATTGCTC	900
Oy	2122	AAGGCGGTGGCATTTATCTCAGAAAGTAAAGTAACTGTGAAAGACATTGTGCTC-GCCT	2180
Db	901	AAAGGCGTGGCATCATATCAGAGGGTAAAGTATGTGAAAGACATTGTGCAAGCCGCGCT	960
Oy	2181	CACATTTCCAGTGAACCAAGT-----GAAACCCAGAGATGCGCAAGGCC-TGTGTAGTAC	2233
Db	961	CACATTTCCAGTGTAAANNMGTCAHHACCCAGAGAACGCGAAGTATGTGTGTGTGTGT	1020
Oy	2234	ATGCGAGTACTTAAAGACATGA-----CCTGTGAAGACTGGATGACATTTTGTGCG	2286
Db	1021	ACGGCTGACCTGAAGACATGANNACATGNNNNNGACACTCGATGATGATCTCTCAAG	1080
Oy	2287	TACCAACAGAGATTTGTCTTTTGTCAAGACCTCTCCCAACAGAAAGCTATCTATGAGG	2346
Db	1081	AACCAACAGAGATGTCTTTGTCTGAACTCTCTCCACAGAGAAAGCTATCTATGTGAGG	1144
Oy	2347	GGCTGCGAGCGAGAGTGTGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2406
Db	1141	GGATGTCAAGAGCAAGGACCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1206
Oy	2407	GCTTGAAGAAAGCAGATATTGGGTTGCTATGGGATTTCTTGTCTGGATGTGTGTGTGT	2466
Db	1201	GCATTGAAGAAAGCTGTGATTTGGATTTGCATGTGGATCTTGTGCTGTACGTCTTAAAG	1266
Oy	2467	CAAGCTGCTGACATGATCTTCTGTGATGACAACTTTGCTTCATCTGTGATCTGGAGTAGA	2526
Db	1261	CAGGAGCGGACATGATCTGT	1326
Oy	2527	GAAAGTCT--GTCTGATATTGTATTAACCTGAAAGAA	2559
Db	1321	GAGGCGCANNGCTGTATCTTTGACAACTTGAAGAAA	1355

RESULT 6
US-09-870-472-12
; Sequence 12, Application US/09870472
; Patent No. US20020095023A1

Best Local Similarity 88.0%; Pred. No. 9.7e-186;
Matches 817; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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QY 1222 GTAGCCAACTGCGGAGAGTTGCTGGCCACGGTACGGTATCTGACGCTCAGCC 1281
Db 1 GTAGCCAACTGCGGAGAGTTGCTGGCCACGGTACGGTATCTGACGCTCAGCC 60
QY 1282 AAGCGCATGCGGAGAGAGTGTGCTGAGAACTGGAAGCTGTGAGAACCTTGGG 1341
Db 61 AAGCGCATGCGGAGAGAGTGTGCTGAGAACTGTGAGAACCTTGGG 120
QY 1342 TCCACATCCACCATCTGCTCCGACAAAGCTGGAACCTGTACTGAAACCGGATGACGTG 1401
Db 121 TCCACATCCACCATCTGCTCCGACAAAGCTGTGAGAACCTGTGAGAACCTTGGG 180
QY 1402 GCTTCACATGAGTGTGACAAATCAATCCATGAACTGACACACAGAGAAATCAGAGTGGG 1461
Db 181 GCTTCACATGAGTGTGACAAATCAATCCATGAACTGACACACAGAGAAATCAGAGTGGT 240
QY 1462 GTCTCTTTTGAAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
Db 241 GTCTCTTTTGAAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 1522 AACAGGCGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581
Db 301 AACAGGCGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 1582 AGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1641
Db 361 AGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 1642 GAGATGAGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1701
Db 421 GAGATGAGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 1702 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1761
Db 481 CAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 1762 GAGGCGCGGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
Db 541 GAGGCGCGGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 1822 CCGCTGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1881
Db 601 CCGCTGAGAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 1882 GAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1941
Db 661 GAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1942 TTCGAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGT 2001
Db 721 TTCGAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGT 780
QY 2002 ATCTCCATGATTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2061
Db 781 ATCTCCATGATTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 2062 GCTGAGATTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2121
Db 841 GCTGAGATTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 2122 AACGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
Db 901 AACGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 928

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RESULT 8
US-10-046-935-809
; Sequence 809, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:

```

; APPLICANT: Jiang, Yugui
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046.935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 809
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 525
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-809

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Query Match 13.4%; Score 486; DB 9; Length 569;
Best Local Similarity 91.0%; Pred. No. 6.3e-117;
Matches 516; Conservative 0; Mismatches 51; Indels 0; Gaps 0.

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QY 2770 GTGAAGAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2829
Db 1 GTGAAGAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 2830 GAGTCTTCTACTTATTTTGTGATTTGTGCTGAGAACGCTTCTCTCTCTCTCTCTCTCTCTCT 2889
Db 61 GAGTCTTCTACTTATTTTGTGATTTGTGCTGAGAACGCTTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 2890 GGCATCCGAGAGAGCTGGGATGACCGCTGATTAATGATGATGATGATGATGATGATGATGATGAT 2949
Db 121 GGCATCCGAGAGAGCTGGGATGACCGCTGATTAATGATGATGATGATGATGATGATGATGATGAT 180
QY 2950 CAGTGGAGCTTACGAGAGAGAGATTTGAGTTTACCTGCGACAGCGCTTCTTCTGTC 3009
Db 181 CAGTGGAGCTTACGAGAGAGAGATTTGAGTTTACCTGCGACAGCGCTTCTTCTGTC 240
QY 3010 AGTATCGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3069
Db 241 AGTATCGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 3070 TTCAGAGAGAGATGAGAGAGAGATTTTATATATTTGACCTCTTTGAGAGAGAGCTCTT 3129
Db 301 TTCAGAGAGAGATGAGAGAGAGATTTTATATATTTGACCTCTTTGAGAGAGAGCTCTT 360
QY 3130 GCTGCTTCTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3189
Db 361 GCTGCTTCTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 3190 CCTACTGAGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3249
Db 421 CCTACTGAGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 3250 CGGAGCTATCATCATGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3309
Db 481 AGGAGCTATCATCATGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 3310 CCGACGCTGCTGAGCGCGCTGGAACAT 3336
Db 541 CCGACGCTGCTGAGCGCGCTGGAACAT 567

```

RESULT 9
US-09-878-178-809
; Sequence 809, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui


```

1 CREATION: Hmt sapiens
2
3 FEATURE:
4
5 NAME/KEY: misc feature
6
7 LOCATION: 100, 137, 383, 395, 411
8
9 OTHER INFORMATION: n A.T.C. 13
10
11 US-10-007-805-271

```

Query Match	11.9%	Score 432.6	DB 12	Length 533
Best Local Similarity	88.0%	Pred. NO.5.3e+03		
Matches 468	Conservative	0	Mismatches 64	Indels 0
				Gaps 0

Dy 150 GAGTGTGATACGATCTTTGGAAAGATTCACTGTGTAAAGTGATGTAAGAGAAATGTGCTTGG 130
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CCAACTTCAACGACATTGTCTTCTTCACACTTAATCTGCATAAAGCATGTGTAAGGAAAAATGTGTTAG 60

D6
27 TGAATGAACTTGAGACCTTGTGGAGACCTTGGCGTCATCAGCCATTGGTTGGCAAGA 1369
|||||
|||
61 TGAGGAATTAGAACTTGTGGAGACCTTGGCGTCATCAGCCATTGGTTGGCAAAA 120

1170 CTGGAAATTTGAAATATATGACAGTGGCTCACTATGTGTTACATCAATCAATTC 1439
1171 CTGCAAGATTTGAAATATATGACAGTGGCTCACTATGTGTTACATCAATCAATTC 180

1430 ATTAAGATGACACTACAGAGAAATAGAAATGTAAGATTTTACAAAGACGTACCAACT 1489
 181 ATGAAGCTGATACACAGAGAAATCAGAGTGTCTCTTTTAAAGAACTTCAGTAACCT 240

Dy 1490 GATTGGTATGAAAGTAATGTATGTTCTACCAACAAGCAGTCATGGAAGA 1544
||| |||||| |
De 741 GATTGATCATGCAATAATGCAGTGCTTATCACCAAGCCATGTTTTAGCGTAAACCAAG 360

Oy	1550	AAAAATTGTTATTTTAACTGTGTGAATAAGTGAGAGAGTAATGGTGGTCTTTTAA	1609
Dd	301	AAAACCTAAGCTATTCTTAAAGAGAGAGAGTGTGAAGAGAGATGCTCAATCTTAA	360

1610 ATGTGATGTGAGGCTTGTGCTGTGCTTGTGATGTGAGATTAAGTAAAGATTAACCAAGATATG 1663
 |||||
 1611 ATGTGATGTGAGGCTTGTGCTGTGCTTGTGATGTGAGATTAAGTAAAGATTAACCAAGATATG 420

Gy 1678 TTTAGATTTCTTCAACTTCACAAAGTGTGAACTTCATTCACAAGAACCCAAAGC 1729
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Ed 421 TCGAGATACTTTTAATTGAATTAACAAAGTCCAGTGTTCTATTTCATAGAAGCCCCAACA 480

QY	1730	CATGGTAACTTAACTAACTTCTATCTATGAAAGGCTGCTCCAGAAAGCATCCT	1781
Db	481	CATGGATTTCTAACTACTGTTGTTGATGAAGGCTGCTCTGAGAAAGCATCTCT	532

RESULT 14
US-09-796-692-8244

Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF
TITLE OF INVENTION: HISTOPATHOLOGICAL MALIGNANCIES

CURRENT APPLICATION NUMBER: US/09/794,602
CURRENT FILING DATE: 2001 03 01
PRIOR APPLICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545

PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779

FACTOR	LOADING	2000	NUMBER	60/000,000
PRICE	APPLICATION			
PRICE	FILING DATE	2000	05	01

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1 PRIC APPLICATION NUMBER: 60/202,084
2 PRIC FILING DATE: 2000-05-09
3 PRIC APPLICATION NUMBER: 60/206,201
4 PRIC FILING DATE: 2000-05-22
5 PRIC APPLICATION NUMBER: 60/218,950
6 PRIC FILING DATE: 2000-07-14
7 PRIC APPLICATION NUMBER: 60/222,903
8 PRIC FILING DATE: 2000-08-03
9 PRIC APPLICATION NUMBER: 60/223,416
10 PRIC FILING DATE: 2000-08-04
11 PRIC APPLICATION NUMBER: 60/223,378
12 PRIC FILING DATE: 2000-08-07
13 NUMBER OF SEQ IDS: 9597
14 SOFTWARE: FASTSEQ for Windows Version 3.0
15 SEQ ID NO 8244
16 LENGTH: 447
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 JS-09-796-692-8244

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Query Match	10.1%	Score 367	DB 9	Length 447
Best Local Similarity	85.8%	Prod. No.	4 5e-85	
Matches 397	Conservative	0	Mismatches 50	Indels 0
				Gaps 0

Cy 1250 CACAGCGTCAAGCTATATTGTGACAGCCTCACTGGTTAAATGATATGCAGTGAATAAATGACTGGCTGG 1309
|||||
|||
Dδ 1 CCACTGTCAAGTGCTGTGTGACACTTAAGTCCAAAAGCATGACCAGGAAAAAACCTGCTTAG 60
|||||
|||

QY	1310 TGAGAGAATCTGSAAGTCTGTGSAAGACCTTGAGTGTTCATCATCAACCATTGTGTGGACAGAGA 1368
Db	61 TGAGAGACTTAGAAGCTGTGTGSAAGACTTTGTGAGTGTCAAGCTCAGCCATCTGTGCTTGATATAAA 120

QY 1370 CTGGAACTCTGACTCAGAACCGGATGACAGTGGCTTACATGTGGTTGGACAACATCAAAATTC 1428

DB 121 CTGGAACTCTGACTCAGAACCGGATGACAGTGGCTTACATGTGGTTGGACAACATCAAAATTC 180

QY 1430 ATGAGCGTGACACCAACAGAGATCAGAGTGGGTCTCCCTTTTACAAACAATTACCTACTT 148

DB 181 ATGAAGCGTGATACGACAGAGAATCTAATAATTCTCTCTTTTTCATTAATAATTTTAGCTATCTT 240

Oy 1490 GGTCTGCTCTGTCCAGAAATTCAGTCTTCTTTTAACTAGGCTTTTCTAGGCTTAACTAAAG 1544
 |||||
 Db 241 GGTTGCTCTGTCCAGAAATTCAGAGTCTTTTAACTAGGCTTTCTAGGCTTAACTAAAG 300

Qy 1550 AAACCTGCGGATGCTTAAAGGCTGACGTACGAGATGCTTCTTTTAA 1608
|||||
|||
Db 301 AAAACCTACTATTCTTAAAGGCGGAGATGCTGACGAGATGCTTCTTTTAA 360
|||||

Oy 1610 AGTGCATCGAGGTTGTGGCTTGTCCTCCTCATGCAACAAATGAACAAGAATGTAATCAAGATTAG 1685
Db 341 ACGCCALANAOCT 420

[illegible]

RESULT 15
CS-03-260-352 6966

PATENT NO. US20020137139A1
GENERAL INFORMATION
APPLICANT: WATSON, WESLEY C

APPLICANT: Byart, John C.
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: NOCETIC ACID AND OTHER MOLECULES ASSOCIATED WITH INFLAMMATION AND

FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-03-24

SEQ ID NO 6966

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2003, 19:39:51 ; Search time 4780 Seconds
(without alignments)
12319.412 Million cell updates/sec

Title: us-10-040-722 3
Perfect score: 3636

Sequence: 1 ggaagctcggcgaggaagga agatgctatctaaagga 3636

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0

Maximum DB seq length: 209090000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hiv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rdi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1889.2	52.0	1846	11	BC013763 Homo sapi
2	1027.8	28.3	1131	11	BC031389 Mus muscu
3	910.8	25.0	1009	11	BC023175 Mus muscu
4	786.8	21.6	935	14	BQ715991 AGENCOURT
5	769.8	21.2	907	14	BQ891199 AGENCOURT
6	767.4	21.1	916	14	BQ900623 AGENCOURT

7	753.6	20.7	895	13	B1904878	603168903
8	752.4	20.7	858	13	B1467185	B1467185
9	751.8	20.7	947	14	BQ231254	BC031254 AGENCOURT
10	744.2	20.5	917	14	BQ943860	BQ943860 AGENCOURT
11	743.6	20.5	883	13	B1102401	B1102401 AGENCOURT
12	738.4	20.3	954	14	BQ714959	BQ714959 AGENCOURT
13	737.2	20.3	1037	14	BW915431	BW915431 AGENCOURT
14	735.4	20.2	933	14	BQ889413	BQ889413 AGENCOURT
15	734.8	20.2	1032	12	BW557903	BW557903 AGENCOURT
16	731.6	20.1	824	13	B1648874	B1648874 AGENCOURT
17	728.4	20.0	945	13	B1524033	B1524033 AGENCOURT
18	725.8	20.0	1057	14	BQ288705	BQ288705 AGENCOURT
19	725.6	20.0	835	13	B1657881	B1657881 AGENCOURT
20	721.6	19.8	893	13	B1660565	B1660565 AGENCOURT
21	720.4	19.8	849	13	B1453217	B1453217 AGENCOURT
22	720.2	19.8	862	13	B1557476	B1557476 AGENCOURT
23	719.6	19.8	1001	13	BW471851	BW471851 AGENCOURT
24	719	19.8	934	14	BQ721757	BQ721757 AGENCOURT
25	718.8	19.8	988	13	BW558808	BW558808 AGENCOURT
26	717.6	19.7	773	13	BQ220975	BQ220975 AGENCOURT
27	717.6	19.7	831	13	B1853043	B1853043 AGENCOURT
28	717	19.7	927	14	BQ677813	BQ677813 AGENCOURT
29	715.6	19.7	976	12	BQ519259	BQ519259 AGENCOURT
30	713.4	19.6	952	14	BQ676875	BQ676875 AGENCOURT
31	713.2	19.6	818	13	B1656053	B1656053 AGENCOURT
32	712.2	19.6	936	13	B1557098	B1557098 AGENCOURT
33	709.8	19.5	1077	13	B1559235	B1559235 AGENCOURT
34	708	19.5	725	14	BQ203256	BQ203256 U1-R-DN1-
35	707	19.4	941	14	BQ676026	BQ676026 AGENCOURT
36	706.8	19.4	923	14	BQ917501	BQ917501 AGENCOURT
37	705.8	19.4	931	13	B1559260	B1559260 AGENCOURT
38	704.8	19.4	708	9	A1598370	A1598370 EST250073
39	704.6	19.4	1071	13	BW560655	BW560655 AGENCOURT
40	704.6	19.4	935	14	BQ940317	BQ940317 AGENCOURT
41	703.6	19.4	935	14	BQ448209	BQ448209 AGENCOURT
42	703.2	19.3	911	14	BQ680281	BQ680281 AGENCOURT
43	703.2	19.3	943	14	BQ950669	BQ950669 AGENCOURT
44	702.6	19.3	1031	13	B1655438	B1655438 AGENCOURT
45	702.4	19.3	943	14	BQ900158	BQ900158 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS BC013763 3846 bp mRNA linear HTC 07-SEP-2001
DEFINITION Homo sapiens, clone IMAGE:3874001, mRNA.
ACCESSION BC013763
VERSION BC013763.1 GI:15489327
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3846)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NHL-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu


```

Db 1971 ATACGGCCAAAGGCATGCGCAAGGAGTGAGGATCATCTCTGAGGCAACGAGACTGTG 2030
Qy 2161 GAAAGATATGCTGCTCCGCTCAGACATTTCCAGTACCGAGGTGAACCCCAAGATGCCAAG 2220
Db 2031 GAGGACATGCGCGCGCGGCTGCAACATTCGCTGACGCGAGGTAAACCCCGGAGATGCAAG 2090
Qy 2221 GCTGTGTAGTACATGAGCATGACTTGAAGAGATGACCTCTGTGAGAGCTGATGACAT 2280
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Qy 2461 TCTAAGAGAGCTGCTGATGATGATTTCTCTGATGACAACTTTGCTCTGATGATGAG 2520
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Qy 2521 GTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
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Qy 2701 CTGGGAGGCTGAGCATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
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Qy 3121 AAGAGCTGTTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
Db 2991 AAGAGCTGTTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3050
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Qy 3241 GACGAGGTGCGGAAGCTCATCATCAGCGAGACGCGCTGAGCGAGCTGAG 3286
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RESULT 2
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LOCUS BC031389
DEFINITION Mus musculus, clone IMAGE:4946041, mRNA.
ACCESSION BC031389
VERSION BC031389.1 GI:21595237
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1131)
REFERENCE
AUTHORS Strausberg, P.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gumaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowals, C.P., Lawrence, S., Martin, P.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 60 Row: C Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis
This clone has the following problem: incomplete processing.
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Query Match 29 3k; Score 1027.8; NP 11; Length 1131;
Best Local Similarity 95.7k; Pred. No. 1.9e-261;
Matches 1069; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

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Db 61 CATTCCGAAATCACCCCTCTGATATTGATTAATGAAGAAATCCATTGCTTAACCTTAACAAG 120
Qy 2646 CACGCTGACCACTCTCTGATTAATGAGGAGATGACATGATGATGATGATGATGATGATGAT 2705

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QY 2951 AGTGAAGCTACGACGAGAGAGAGATTGTGAGTTACCTTGGCACAGCGCTTTCTTTGTCA 3010
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 QY 3011 GATTCGTGAGTGCAGTGGGCTGACTTGTGCATCTGCAAGACCAAGAGAAATCTGTCT 3070
 Db GATTCGTGAGTGCAGTGGGCTGACTTGTGCATCTGCAAGACCAAGAGAAATCTGTCT 420
 QY 3071 TCCAGAGAGAGAGAGAGAGAGATCTTAAATATTTGGCTTTTGAAGAGACAGCTCTTG 3130
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 QY 3251 GGAAGCTCATATCAGAGCGAGCGCTGGGCTGGGTGGAGAGAGAACTTACTATGCTGC 3310
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 QY 3485 AGGCTGCGCGCGAG 3544
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 QY 3545 TTGTTGTTTGTAAAG 3604
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 QY 3605 TTTTACAATTAAGATGGCTATTATACGAA 3636
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 5', mRNA sequence.
 ACCESSION B0715991
 VERSION B0715991.1 GI:21854890
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 935)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@pds-remail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.
 cDNA Library Preparation: Resgen, Invitrogen Corp.
 DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLNL3730 row: 0 column: 12
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 Location/Qualifiers
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 /note="Organ: olfactory epithelium; Vector: pcwv-SPORE6.1.cdb; Site 1: EFORV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH-MGC Library."
 BASE COUNT 227 a 240 c 251 g 216 t 1 others
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 Query Match 21.6%; Score 786.8; DB 14; Length 935;
 Best Local Similarity 93.3%; Pred. No. 1.8e-197;
 Matches 854; Conservative 0; Mismatches 58; Indels 3; Gaps 3;
 QY 2183 ACATTCAGTGAACCGAGTGAACCCAGAGATGCCAAGCGCTGTGATACATGGCAGTG 2242
 Db ACATTCAGTGAACCGAGTGAACCCAGAGATGCCAAGCGCTGTGATGTCAGCGTATG 60
 QY 2243 ACTGAAGACATGAACCTGTGAAGAGCTGATGATTTTGGGTACACACAGAGATTTG 2302
 Db ACTGAAGACATGAACCTGTGAAGAGCTGATGATTTTGGGTACACACAGAGATG 120
 QY 2303 TCTTTGTAGAGCTTCTCTCAAGAGAGCTCATATTGTGAGAGGCTGCGAGCGGAG 2362
 Db TCTTTGTAGAGCTTCTCTCAAGAGAGCTCATATTGTGAGAGGCTGCGAGCGGAG 180
 QY 2363 GTGCCATGTGCTGTGTCAGAGGAGTGTGTCATGACTCTCCAGCTTTGAAGAGAGAG 2422
 Db GTGCCATGTGCTGTGTCAGAGGAGTGTGTCATGACTCTCCAGCTTTGAAGAGAGAG 240
 QY 2423 ATATTGGGAGTGGCCATGAGGAGATTTGTGCTGGATGTGTCAGAGAGAGCTGTGATGA 2482
 Db ATATTGGGAGTGGCCATGAGGAGATTTGTGCTGGATGTGTCAGAGAGAGCTGTGATGA 300
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 Db TTGATTAAGTGAAGAGATCCATTGCTTACACCTTAACAAGTAACTTCCGGAATCACCC 420
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 Db CCTCTTGATATTTATTTATTTGCAAACTTCACTGCTGCTGGGACCGTGACATCTCT 480
 QY 2663 GCATGACTTGGGAGCTGACATGATGCTCCGCCATCTCTGCGGCTTGAACAGAGCTGAAA 2722
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 Db GTGACATCATGAAG 600
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CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13744 row: 1 column: 09
 High quality sequence stop: 607.

FEATURES

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 /note="Organ: olfactory epithelium; Vector:
 pCMV-SPORT6.1.cdb; Site_1: EcoRI; Site_2: NotI; Cloned
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 2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this
 is a NIH MGC library."
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 Best Local Similarity 92.7%; Pred. No. 2.6e-192;
 Matches 849; Conservative 0; Mismatches 62; Indels 5, Gaps 4;

1756 ATGAAGGCGCCCGAGAAAGATCTGACGATGAGCTTATCTCCCTCCAGCGGCAAG 1815
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 1816 GACACAGCCCTGAGCAAGAGCTGAGAGAGCCCTTTCAGAAATGCTTACTAGAGCTGGG 1875
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 2296 GAGATTTCTTTGCTAGAGCTCTCTCAAGAGAGATCATTTGTGAGAGGCTGGCAG 2355
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 DB 781 GTCGATATTTGATTAACCTGAGAAAT-CATCGCTTACACCTTAACAAGTAACTCCGG 839
 QY 2594 AAATACCCCTTTGATTAATTTATTTGCAACATTTCACTGCCCC--TGCGACCGT 2651
 DB 840 AAATACCCCTTTGATTAATTTATTTGCAACATTTCCCTGCCCCGCGAGCTGTG 899
 QY 2652 GACCATCTCTGCAAT 2667
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RESULT 7
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 LOCUS 603168903F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256937 5',
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 mRNA sequence.
 ACCESSION BI904878
 VERSION BI904878.1 GI:16167292
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 895)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1649 row: e column: 02
 High quality sequence start: 58
 High quality sequence stop: 893.
 Location/Qualifiers

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 /tissue_type="pooled lung tumors"
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 lung tumors with a Not I - oligo(dAT) primer [5']
 TCTTACCAATCTGAAGTGGAGCGCGCGCTCTGTTTTTTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pRT30 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 211 a 237 c 245 g 232 t
 ORIGIN

Query Match 20.7%; Score 753.6; DB 13; Length 895;
 Best Local Similarity 94.0%; Pred. No. 1.2e-188;
 Matches 805; Conservative 0; Mismatches 49; Indels 2, Gaps 2;

Db 434 GGAATGAAAGAAATCTTATATATTTGACCTCTTTGAGAGACAGCCCTTGCTGCTTTC 493
 QY 3139 CTGCTCTACTGCTCCGGATGGTGAGCCCTTATAGATGATCCCTCAAACTACTTGG 3198
 Db 494 TTATCTTACTGCTCCGGATGGTGAGCCCTTATAGATGATCCCTCAAACTACTTGG 553
 QY 3199 TGGTTTGTGCTCTTCCCTTACCTCTTCTGATCTTGTATGAGAGAGAGAGCTC 3258
 Db 554 TGGTTTGTGCTCTTCCCTTACCTCTTCTGATCTTGTATGAGAGAGAGAGAGCTC 613
 QY 3259 ATCATGAGGAG 3318
 Db 614 ATTAT 673
 QY 3319 CTGACAGCCGCTGAGAGATTTGCTACACACTGACAGCTACAGCTACAGCTTGTATC 3378
 Db 674 CTGACAGCCGCTGAGAGATTTGCTACACACTGACAGCTACAGCTACAGCTTGTATC 733
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RESULT 9
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 ACCESSION BQ931254
 VERSION BQ931254.1 GI:22346285
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 947)
 NIH-MGC http://mgs.nci.nih.gov/.

REFERENCE
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: CGAP@fmail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
 Plate: LLM1388 row: n column: 05
 High quality sequence stop: 607.

FEATURES
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 Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 205 a 254 c 262 g 216 t 10 others
 ORIGIN

Query Match 20.7%; Score 751.8; DB 14; Length 947;
 Best Local Similarity 91.1%; Pred. No. 3.7e-188;
 Matches 856; Conservative 0; Mismatches 70; Indels 14; Gaps 5;

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 QY 2660 TCTGCAATTGACTTGGGACATGACATGGTTCGGGCACTCTCTTGCCCTATGAAACAGCTG 2719
 Db 67 TCTGCAATTGACTTGGGACATGACATGGTTCGGGCACTCTCTTGCCCTATGAAACAGCTG 126
 QY 2720 AAAGTGACATCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2779
 Db 127 AGAGCGACATCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
 QY 2780 GTCGATCAGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2839
 Db 187 GTCGATCAGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 246
 QY 2840 CTATATTTTGTGATTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2899
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 QY 2900 AAGCTCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2959
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 Db 367 ACAGCAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 426
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 Db 487 GAATGAAGAAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 546
 QY 3140 TGTCTACTGCTCCCTGGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3198
 Db 547 TGTCTACTGCTCCCTGGAGATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
 QY 3199 TGGTTTGTGCTCTTCCCTTACTCCCTCTCATCTTCTGTATGAGAGAGAGAGAGAGAG 3258
 Db 607 TGGTTTGTGCTCTTCCCTTACTCCCTCTCATCTTCTGTATGAGAGAGAGAGAGAGAG 666
 QY 3259 ATCATGAG 3317
 Db 667 ATCATGAG 726
 QY 3318 CTGACAGCCGCTGAGAGATTTGCTACACACTGACAGCTACAGCTACAGCTTGTATC 3376
 Db 727 CTGACAGCCGCTGAGAGATTTGCTACACACTGACAGCTACAGCTACAGCTTGTATC 786
 QY 3377 ACTTCAAGTCTTGGAGCTGAGAGATTTGCTACAGCTACAGCTACAGCTACAGCTTGTATC 3435
 Db 787 ACTTCAAGTCTTGGAGCTGAGAGATTTGCTACAGCTACAGCTACAGCTACAGCTTGTATC 846
 QY 3436 ATTCAGAGCTCTGAGATGAGAGATTTGCTACAGCTACAGCTACAGCTACAGCTTGTATC 3485
 Db 847 ATTCAGAGCTCTGAGATGAGAGATTTGCTACAGCTACAGCTACAGCTACAGCTTGTATC 906
 QY 3486 GGGCTGCGGAG 3525
 Db 907 GGGCTTCTCTGAG 946

RESULT 10
 BQ943860 917 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT 8801902 NCI_CGAP_Mam2 Mus musculus cDNA clone
 DEFINITION IMAGE:6439036 5', mRNA sequence.
 ACCESSION BQ943860
 VERSION BQ943860.1 GI:22359338
 KEYWORDS EST.

Query Match	20.5%	Score 743.6	DB 13	Length 883
Best Local Similarity	93.4%	Pred. No. 5.4e-186		
Matches 820	Conservative 0	Mismatches 54	Indels 4	Gaps 4
QY 2199	GGTCGACCCCGAGATGCCCAAGGCGCTGTAGTACATGGC.AGTGACTTGAAGACATGA	2257		
Db 1	GGTGAACCCCGAGATGCCCAAGGCGCTGTAGTGTCCACGGCGAGTGAACCTGAAGACATGA	60		
QY 2258	CGTCTGAGAGAGCTGGATGACATTTTGGGGTAAACACAGAGAAATTTGTCTTGTAGAACTT	2317		
Db 61	CGTCGGAGAGAGCTGGATGACATTTTGGGGTAAACACAGAAATTTGTCTTGTAGAACTT	120		
QY 2318	CTGCGTCAACAGAAAGCTCATATTGTGAAAGAGGCTGACAGGCGAGAGGCTGATGAGCTG	2377		
Db 121	CTCTCTGAGCAGAAAGCTCATATTGTGAAAGAGGCTGACAGGCGAGAGGCGCATCTGTGCGG	180		
QY 2378	TCAACAGGGATGGTGTCAATGACTCTCCAGCTTTGAAAAAGCAGATATTGGGGTTGCCA	2437		
Db 181	TCACAGGGAGTGGTGTCAATGACTCTCCAGCTTTGAAAAAGCAGATATTGGGGTTGCCA	240		
QY 2438	TGGGGATTGTGGGTGGAGTGTGCCAAGCAAGGTGGTGCATGATATCTTGTGATGCA	2497		
Db 241	TGGGGATTGTGGGTGGAGTGTGCCAAGCAAGGTGGTGCATGATATCTTGTGATGCA	300		
QY 2498	ACTTTGCTCCATCTGTAAGTGAAGAAAGTGTCTGATATTGGTAACTTGAAGA	2557		
Db 301	ACTTTGCTCCATCTGTAAGTGAAGAAAGTGTCTGATATTGGTAACTTGAAGA	360		
QY 2558	AATTCATTGCTTACACCCCTAACAGAAATCATTCCGGAAATCAACCCCTTTCTTATTTTA	2617		
Db 361	AATTCATTGCTTACACCCCTAACAGAAATCATTCCGGAAATCAACCCCTTTCTTATTTTA	420		
QY 2618	TTATTTGAACATTCCACTGCGCCGTGGGCAACGGAGCATCTCTGCAATTGACTTGGGCA	2677		
Db 421	TTATTTGAACATTCCACTGCGCCGTGGGCAACGGAGCATCTCTGCAATTGACTTGGGCA	480		
QY 2678	CTGACATGGTTCGCCGCAATCTCTGACCTATGAAACAGCTGAAAGTACATCATGAAGA	2737		
Db 481	CTGACATGGTTCGCCGCAATCTCTGACCTATGAAAGCAAGTGAAGGACATCATGAAGA	540		
QY 2738	GGCAGCCAGAAATCCCAAAACGGACAACTTTGACAGAGGCTTGATCAGCATGCGCT	2797		
Db 541	GGCAGC-CCAGAAACCCCAAAACGGACAACTTTGACAGAGGCTTGATCAGCATGCGCT	599		
QY 2798	ATGCAACGATGGTATGATCCAGAGCGCTGGAGGCTTCTTCACTATATTGGATTGTGG	2857		
Db 600	ATGCAACGATGGTATGATCCAGAGCGCTGGAGGCTTCTTCACTATATTGGATTGTGG	659		
QY 2858	CTGAGAACGGTTTCTGCGCTTCACTGTTGGGATCCGAGAGACCTGGATGACCGCT	2917		
Db 660	CTGAGAACGGTTTCTGCGCTTCACTGTTGGGATCCGAGAGACCTGGGATGACCGCT	719		
QY 2918	GGATTAAATGATGTGAGAGACAGCTACGGGACAGAGTGAACCTACAGACAGAGAGAAATTG	2977		
Db 720	GGATTAAATGATGTGAGAGACAG-TCAGGACACAGATGACCTACAGACAGAGAGAAATTG	778		
QY 2978	TGAGATTACCTGGCAGACGGGCGCTTCTTTGTAGATGATGGGTAGTGCAGTGGCGTCACT	3037		
Db 779	GGAGATTACCTTTGTATATCAG-GTTCTTTTGTAGATATGATGGGTATGACGATGGGCGAAT	837		
QY 3038	TGGTCATCTGCAAGACAGAAAGAAATCTGTCTTCAG	3075		
Db 838	TGGTCATCTGCAAGACCAAAAGAAATCTGTCTTCACAG	875		
RESULT 12				
LOCUS	B0714959	954 bp	mRNA	linear
DEFINITION	AGNCACOURT 8482883 NIH_MGC_129 Mus musculus cDNA clone IMAGE:63060767			
ACCESSION	B0714959			
VERSION	B0714959.1	GI:21853858		

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 954)
JOURNAL	NIH-MGC http://imgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov . Tissue Procurement: Susan L. Sullivan, PhD. cDNA Library Preparation: Resgen, Invitrogen Corp. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM31721 Row: g Column: 05 High quality sequence stop: 625. Location/Qualifiers 1. 954 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:6306076" /clone_id="NIH_MGC_129" /lab_host="DH10B (phage-resistant)" /note="Organ: olfactory epithelium; Vector: pCMW-SPOB6.1.cdb; Site:1; ECOV; Site_2: NotI; Cloned directionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this is a NIH-MGC library."
BASE COUNT	233 a 262 c 256 g 203 t
ORIGIN	
Query Match	20.3%; Score 738.4; DB 14; Length 954;
Best Local Similarity	88.9%; Pred. No. 1.3e-184;
Matches 846; Conservative	0, Mismatches 96; Indels 10; Gaps 4;
QY	1276 ACTGCCAAGCGCGATGGCAGAGAGAAGACTGCTCGTGGAGAACTCGGAAGCGTGTGAGAGAC 1335
Db	1 ACTGCCAAGCGCGATGGCAGAGAGAAGACTGCTCGTGGAGAACTCGGAAGCGTGTGAGAGAC 60
QY	1336 TTGGGGGTCACATCCACCATCTGCTCCGACAGAGATGGAACTCTGACTCAGAACCGGATG 1395
Db	61 TTGGGGGTCACATCTACCATCTGCTCCGACAGAGATGGAACTCTGACTCAGAACCGGATG 120
QY	1396 ACAGTGGCTCATGTGGTTTGACAAATCCATGAACTGACACCAAGAGATGAG 1455
Db	121 ACAGTGGCCCATGTGGTTTGACAAATCCATGAACTGACACCAAGAGATGAG 180
QY	1456 AGTGGGCTCTCTTTGACAAAGCGTACCAACCTGTCGCTCTGTCAGAAATTCCTGCT 1515
Db	181 AGTGGTGTCTCTTTGACAAAGCGTACCAACCTGTCGCTCTGTCAGAAATTCCTGCT 240
QY	1516 CTCTGTAAACAGGCGAGTGTTCAGGCTAACCAAGAAACCTGCTTACCTTAAGCTGCA 1575
Db	241 CTCTGTAAACAGGCGAGTGTTCAGGCTAACCAAGAAACCTGCTTACCTTAAGCGGCA 300
QY	1576 GTACGGCGAGATGCTTTCCGAGTCGGCGCTCTTAAGTCATGTGAGAGTCTGTGTGAGTTC 1635
Db	301 GTACGGCGAGATGCTCTGAGTCGGCGCTCTTAAGTCATGTGAGAGTCTGTGTGAGTTC 360
QY	1636 GTGATGCGATGAGGAGAGAGTACCAAGATAGTGGAGATTCCTCTTCAACTCCACCAAC 1695
Db	361 GTGATGCGATGAGGAGAGATAGCAAGATAGTGGAGATTCCTCTTCAACTCCACCAAC 420
QY	1696 AAGTACCAAGCTCTCATTTACAAAGACCAACGATCGAGCCTTAAGCACTGTGTAAGT 1755
Db	421 AAGTACCAAGCTTCTCATTTACAAAGACCAACGATCGAGCCTTAAGCACTGTGTAAGT 480
QY	1756 ATGAAGGGGGCCCCAGAAAGATCTCGAGCCGATCGAGTTCTATCTCTCCACCGCAAG 1815

[illegible][illegible]

RESULT 14
 B0889413
 LOCUS
 DEFINITION AGENCOURT_8728430 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5339047
 5', mRNA sequence.
 ACCESSION B0889413
 VERSION B0889413.1 GI:22281427
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 933)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM2533 row: d column: 24
 High quality sequence stop: 691.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:5339047"
 /tissue_type="NIH MGC 47"
 /lab_host="DH10B (phage-resistant) cell line"
 /note="Organ: brain; Vector: pOT87; Site: 1: XhoI; Site: 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH MGC Library."
 BASE COUNT 239 a 217 c 234 g 239 t 4 others
 ORIGIN
 Query Match 20.2%; Score 735.4; DB 14; Length 933;
 Best Local Similarity 88.8%; Pred. No. 8.3e-184;
 Matches 793; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Db 304 CACTGGGATCGCACTGTGATGGGAAGATTGCGACACTTGCTTGGGCTGAAGAGAG 363
 QY 1077 CCGACCCCATGCTGTAAGAAATCGAGCACTTATCCACTCTCTACGAGGCTGGCCGT 1136
 Db 364 CGAGACCCCATGCTGCAAAATGGAACATTTATCCATCATACAGGAGTGGCTGT 423
 QY 1137 GTTCCGAGGAGTGTCTTCTTCAATCTCTCTGATCCTTGAATCACTGAGCTGAGAG 1196
 Db 424 GTTCCGAGGAGTGTCTTCTTCAATCTCTCTGATCCTTGAATCACTGAGCTGAGAG 483
 QY 1197 TGTGATCTTCTCATTTGATATCATGTCAGCAACGTCGCGAAGTTTGTGCGCCAGCT 1256
 Db 484 TGTGATCTTCTCATTTGATATCATGTCAGCAACGTCGCGAAGTTTGTGCGCCAGCT 543
 QY 1257 CAGGATGCTGACCTCTCTGCAAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1316
 Db 544 CAGGATGCTGACCTCTCTGCAAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603
 QY 1317 CCGGAAGCTGTGAGAGCTTGGGGTCCACATCCACATCTGCTCCGACAGACTGAGAC 1376
 Db 604 CTTAGAAAGCTGTGAGAGCTTGGGGTCCACATCCACATCTGCTCCGACAGACTGAGAC 663
 QY 1377 TGTGATCTGAGACCGGATGACAGTGTGCTCATATGCTTTGACATCAATTCATGAGAG 1436
 Db 664 TGTGATCTGAGACCGGATGACAGTGTGCTCATATGCTTTGACATCAATTCATGAGAG 723
 QY 1437 TGACACACAGAAATGAGTGGGGTCTCTTGAACAAGAGCTGACCTGCTGCTGGC 1496
 Db 724 TGATAGACAGAAATGAGTGGGGTCTCTTGAACAAGAGCTGACCTGCTGCTGGC 783
 QY 1497 TGTGATCTGAGATGCTGCTCTGTAACAGGAGCTTTGAGCTAAACAGAAAGCT 1556
 Db 784 TGTGATCTGAGATGCTGCTCTGTAACAGGAGCTTTGAGCTAAACAGAAAGCT 843
 QY 1557 GCTATCTTAAAGCTGAGTACGCGAGATGCTTCCGAGTGGGCTTTAA 1609
 Db 844 ACCTATTTCTTAAAGCTGAGTACGCGAGATGCTTCCGAGTGGGCTTTAA 996

RESULT 15
 BMS57003
 LOCUS
 DEFINITION AGENCOURT_6578791 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5465507
 5', mRNA sequence.
 ACCESSION BMS57003
 VERSION BMS57003.1 GI:18798681
 KEYWORDS EST.
 SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1032)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM1967 row: a column: 04
 High quality sequence stop: 726.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:5465507"
 /clone_lib="NIH_MGC_41"
 /tissue_type="amelanotic melanoma, cell line"

